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SEARCH REQUEST FORM

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If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

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Searcher: <u>R. Schreiber</u>	NA Sequence (#) _____	STN _____
Searcher Phone #: <u>308-4292</u>	AA Sequence (#) <u>1</u>	Dialog _____
Searcher Location: <u>CM1 12E19</u>	Structure (#) _____	Questel/Orbit _____
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41622

STIC-Biotech/ChemLib

From: Seharaseyon, Jegatheesan
Sent: Wednesday, May 02, 2001 3:59 PM
To: STIC-Biotech/ChemLib
Subject: Re:09/467160

Please search the commercial database for SEQ ID:3 of 09/467,160. Thanks.

J.Seharaseyon
Art Unit 1647
CM1 10D16
10CO1 MB
(703)-305-1112

GenCore version 4.5
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OM protein - protein search, using sw model

Run On: May 4, 2001, 07:35:28 ; Search time 18.57 Seconds
(without alignments)
224.713 Million cell updates/sec

Title: US-09-467-160-3

Perfect score: 379

Sequence: 1 APLATELRCCLOTTLOGIHL.....PASPMPVKKIIEKMLKNGKSN 73

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0401.*

- 1: /SID56/gcgdata/geneseq/geneseq/AA1980.DAT.*
- 2: /SID56/gcgdata/geneseq/geneseq/AA1981.DAT.*
- 3: /SID56/gcgdata/geneseq/geneseq/AA1982.DAT.*
- 4: /SID56/gcgdata/geneseq/geneseq/AA1983.DAT.*
- 5: /SID56/gcgdata/geneseq/geneseq/AA1984.DAT.*
- 6: /SID56/gcgdata/geneseq/geneseq/AA1985.DAT.*
- 7: /SID56/gcgdata/geneseq/geneseq/AA1986.DAT.*
- 8: /SID56/gcgdata/geneseq/geneseq/AA1987.DAT.*
- 9: /SID56/gcgdata/geneseq/geneseq/AA1988.DAT.*
- 10: /SID56/gcgdata/geneseq/geneseq/AA1989.DAT.*
- 11: /SID56/gcgdata/geneseq/geneseq/AA1990.DAT.*
- 12: /SID56/gcgdata/geneseq/geneseq/AA1991.DAT.*
- 13: /SID56/gcgdata/geneseq/geneseq/AA1992.DAT.*
- 14: /SID56/gcgdata/geneseq/geneseq/AA1993.DAT.*
- 15: /SID56/gcgdata/geneseq/geneseq/AA1994.DAT.*
- 16: /SID56/gcgdata/geneseq/geneseq/AA1995.DAT.*
- 17: /SID56/gcgdata/geneseq/geneseq/AA1996.DAT.*
- 18: /SID56/gcgdata/geneseq/geneseq/AA1997.DAT.*
- 19: /SID56/gcgdata/geneseq/geneseq/AA1998.DAT.*
- 20: /SID56/gcgdata/geneseq/geneseq/AA1999.DAT.*
- 21: /SID56/gcgdata/geneseq/geneseq/AA2000.DAT.*
- 22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	379	100.0	73	14 R36771	MIP-2alpha. Homo
2	379	100.0	73	16 R66699	Human gro-beta che
3	379	100.0	73	18 W18025	Human chemokine gr
4	379	100.0	73	18 W17671	Human chemokine gr
5	379	100.0	73	20 Y18104	Human gro-beta pro
6	379	100.0	73	20 W81499	Human gro-beta pol
7	379	100.0	73	21 Y69036	Amino acid sequenc
8	379	100.0	107	13 R20590	Human macrophage i
9	379	100.0	107	13 R20529	Human macrophage i
10	379	100.0	107	13 R23034	Human Gro beta cyt
11	379	100.0	107	20 W96714	Growth related onc

12	379	100.0	107	21 B15810	Human chemokine GR
13	352	92.9	102	16 R70793	Gro-beta/MIP-2- α p
14	331	87.3	73	16 R66698	Human gro-alpha ch
15	331	87.3	73	18 W18024	Human chemokine gr
16	331	87.3	73	18 W17670	Human chemokine gr
17	331	87.3	73	20 Y18106	Human gro-alpha pr
18	331	87.3	73	20 W81498	Human mature gro-a
19	331	87.3	73	21 Y69026	Amino acid sequenc
20	331	87.3	107	20 W96713	Growth related onc
21	331	87.3	107	21 B15793	Human chemokine GR
22	331	87.3	107	21 B15813	Human chemokine GR
23	330	87.1	107	16 R70792	Melanoma growth st
24	325	85.8	73	14 R36772	MIP-2beta. Homo s
25	325	85.8	73	16 R66700	Human gro-gamma ch
26	325	85.8	73	17 R93194	Protein used to ge
27	325	85.8	73	18 W18026	Human chemokine gr
28	325	85.8	73	20 Y18107	Human gro-gamma pr
29	325	85.8	73	20 W81500	Human mature gro-g
30	325	85.8	73	21 Y69037	Amino acid sequenc
31	325	85.8	106	13 R23035	Human Gro gamma cy
32	325	85.8	106	20 W96715	Growth related onc
33	325	85.8	107	13 R20590	Human macrophage i
34	325	85.8	107	16 R70794	Gro-gamma/MIP-2-be
35	323	85.2	73	18 W17672	Human chemokine gr
36	318	83.9	107	13 R20530	Human macrophage i
37	284	74.9	72	12 R14077	Cytokine and neutr
38	283	74.7	73	18 W12434	Chimeric interleuk
39	278	73.4	72	16 R66697	Mouse KC chemokine
40	278	73.4	72	18 W18023	Murine chemokine K
41	278	73.4	72	18 W17669	Murine chemokine K
42	278	73.4	72	20 Y18105	Murine protein KC
43	278	73.4	72	20 W81497	Mouse mature KC po
44	267.5	70.6	72	18 W12436	Chimeric interleuk
45	261	68.9	100	11 R05790	Macrophage derived

ALIGNMENTS

RESULT	1
R36771	ID R36771 standard; protein; 73 AA.
AC	AC R36771;
XX	XX
DT	DT 29-SEP-1993 (first entry)
XX	XX MIP-2alpha.
DE	DE Macrophage inflammatory protein; megakaryocytopoiesis; MIP-1; MIP-2;
KW	KW thrombocythemia; reactive thrombocytosis; stroke; emboli; platelet;
KW	KW myeloproliferative disorder.
XX	XX Homo sapiens.
OS	OS
XX	XX WO9309799-A.
PN	PN
XX	XX 27-MAY-1993.
XX	XX
PF	PF 13-NOV-1992; 92WO-US09671.
XX	XX
PR	PR 15-NOV-1991; 91US-0792988.
PA	PA (UYPE-) UNIV PENNSYLVANIA.
XX	XX Gewirtz AM;
PI	PI
XX	XX WPI; 1993-182239/22.
DR	DR
XX	XX Suppression of megakaryocytopoiesis - by administration of
PT	PT macrophage inflammatory protein-1 or -2
XX	XX
PS	PS Disclosure; Page 18; 26pp; English.

XX A claimed method for reducing the no. of circulating platelets in the
 CC bloodstream of a mammal comprises admin. of MIP-1 and/or MIP-2 or
 CC their analogues to induce such a reduction. The MIP-1, MIP-2 or
 CC analogue may be operatively linked to a carrier. The MIPs can be
 CC used to inhibit megakaryocytopoiesis to effect in vivo reduction of
 CC platelet nos. They can be used to treat disorders with excessively
 CC high platelet counts such as thrombocytosis, stroke, pulmonary emboli
 CC and myeloproliferative disorders.
 XX
 SQ Sequence 73 AA;

Query Match 100.0%; Score 379; DB 14; Length 73;
 Best Local Similarity 100.0%; Pred. No. 1.4e-38;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APLATELRCCLOTLQGIHLKNIQSVKSPGPHCAQTEVIATLKNGQKACLNPA^{SP}PMVK 60
 DB 1 APLATELRCCLOTLQGIHLKNIQSVKSPGPHCAQTEVIATLKNGQKACLNPA^{SP}PMVK 60
 DB 61 KIIEKMLKNGKSN 73
 61 KIIEKMLKNGKSN 73

RESULT 2
 ID R66699 standard; protein; 73 AA.
 XX R66699;
 AC R66699;
 XX 19-JUL-1995 (first entry)
 DT Human gro-beta chemokine.
 XX Gro-alpha protein; chemokine; inflammation; antiinflammatory;
 KW hematopoietic synergistic factor; HSF; hematopoietic precursor;
 KW bone marrow; intercrine; desamino gro-beta; truncation.
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Protein 5..73
 FT /note= "desamino truncated gro-beta, claim 6,
 FT page 58"
 XX WO9429341-A.
 XX 22-DEC-1994.
 XX 03-JUN-1994; 94WO-US06264.
 XX 08-JUN-1993; 93US-0073800.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 XX Balcarek JM, Bhatnagar P, King AG, Pelus LM;
 XX WPI; 1995-036402/05.
 XX New truncated chemokine with increased biological activity - and
 XX related multimers, nucleic acid, antibodies etc., for treating
 XX inflammation, stimulating growth of bone marrow etc., also
 XX peptide(s) for inducing haematopoietic synergistic factor.
 XX Disclosure; Page 51-52; 89pp; English.
 XX Truncated, desamino chemokine comprising amino acids 5-73 of
 CC human mature gro-beta (full sequence given in R66699)
 CC shows enhanced biological activity when compared to the mature
 CC protein, and has been used to prepare multimeric, modified
 CC chemokines.

XX Sequence 73 AA;
 SQ

Query Match 100.0%; Score 379; DB 16; Length 73;
 Best Local Similarity 100.0%; Pred. No. 1.4e-38;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APLATELRCCLOTLQGIHLKNIQSVKSPGPHCAQTEVIATLKNGQKACLNPA^{SP}PMVK 60
 DB 1 APLATELRCCLOTLQGIHLKNIQSVKSPGPHCAQTEVIATLKNGQKACLNPA^{SP}PMVK 60
 QY 61 KIIEKMLKNGKSN 73
 DB 61 KIIEKMLKNGKSN 73

RESULT 3
 ID W18025 standard; protein; 73 AA.
 XX W18025;
 AC W18025;
 XX 30-JAN-1998 (first entry)
 DT Human chemokine gro beta.
 XX Human chemokine gro beta.
 XX Sepsis; septic shock; therapy; gro beta; chemokine; human.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT Protein 5..73
 FT /note= "preferred modified fragment of KC
 FT (Claim 2)"
 XX WO9719173-Al.
 XX 29-MAY-1997.
 XX 20-NOV-1996; 96WO-US18616.
 XX 21-NOV-1995; 95US-0007425.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 XX DeMarsh PL, Johanson KO;
 XX WPI; 1997-298111/27.
 XX Use of chemokine(s) such as KC and gro-alpha - to treat or prevent
 XX sepsis, particularly septic shock
 XX Claim 1; Page 19; 28pp; English.
 XX A claimed method of treating or preventing sepsis comprises
 XX administering to an animal an effective amount of a chemokine
 XX selected from mature murine KC (see W18023), human gro alpha (see
 XX W18024), human gro beta (W18025) and human gro gamma (see
 XX W18026), modified fragments of these chemokines and multimeric
 XX proteins comprising an association of two chemokine proteins.
 XX Sepsis can occur in hospitalised patients, and a consequence of
 XX bacterial sepsis is septic shock. The method of the invention
 XX provides a treatment for sepsis, particularly septic shock, which
 XX is a major cause of death in intensive care units. Septic shock
 XX syndrome apparently has intractable resistance to the effects of
 XX a variety of highly potent antimicrobial agents. Survival is
 XX increased by treatment with the chemokines, both prophylactically
 XX and after infection.
 XX Sequence 73 AA;
 SQ

XX	Y69036;
XX	AC
XX	KW
DT	DT
XX	DE
DE	30-MAY-2000 (first entry)
XX	Amino acid sequence of chemokine receptor ligand MIP-2alpha.
XX	Chemokine receptor; ligand; inflammatory response; immune effector cell;
KW	secondary tissue damage; central nervous system injury; MIP-2alpha;
KW	CNS inflammatory disease; neurodegenerative disorder; heart disease;
KW	inflammatory eye disease; inflammatory bowel disease;
KW	inflammatory joint disease; inflammatory kidney; renal disease;
KW	inflammatory lung disease; inflammatory nasal disease;
KW	inflammatory thyroid disease; thyroiditis; cytokine-regulated cancer.
XX	Homo sapiens.
OS	OS
XX	WO200004926-A2.
PN	XX
PD	03-FEB-2000.
XX	21-JUL-1999; 99WO-CA00659.
PF	XX
XX	22-JUL-1998; 98US-0120523.
PR	XX
XX	(OSPR-) OSPREY PHARM LTD.
PA	McDonald JR, Coggins PJ;
XX	WI; 2000-182542/16.
DR	XX
PT	A new therapeutic agent comprising a conjugate for treating secondary
PT	tissue damage and other disease conditions like Alzheimer's disease,
PT	stroke, Parkinson's disease and atherosclerosis
XX	Disclosure; Page 60; 204pp; English.
PS	The present sequence represents a chemokine receptor ligand. The present
XX	ligand can be incorporated into the conjugates of the invention. The
CC	specification describes a conjugate, comprising a targeted agent and a
CC	chemokine receptor ligand. The conjugate binds to a chemokine receptor
CC	resulting in internalisation of the targeted agent in cells bearing the
CC	receptor. The conjugates are used for formulating a medicament or for
CC	treating disorders associated with inflammatory responses resulting from
CC	activation, proliferation and migration of immune effector cells. The
CC	disorders or disease states comprise secondary tissue damage such as
CC	central nervous system (CNS) injury, CNS inflammatory diseases,
CC	neurodegenerative disorders, heart disease, inflammatory eye diseases,
CC	inflammatory bowel diseases, inflammatory joint diseases, inflammatory
CC	kidney or renal diseases, inflammatory lung diseases, inflammatory
CC	nasal diseases, inflammatory thyroid disease such as thyroiditis, or
CC	cytokine-regulated cancers.
XX	Sequence 73 AA:
SQ	Query Match 100.0%; Score 379; DB 21; Length 73;
	Best Local Similarity 100.0%; Pred. No. 1 4e-38;
	Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 APLATELRCQCLOTLQGIIHLNKIOSVKVSPGPHCAQTVEIATLNKGOKACINLPASPMVK 60
Db	1 aplatelrcqcqlqgiihlkngskvkspgphcaqtveiatlknqgkacinpaspvk 60
OY	61 KIEEKMLKNGKSN 73
Db	61 kilekmikngksn 73
RESULT	8
R20589	ID R20589 standard; Protein; 107 AA.
XX	XX

AC R20589;
 XX 23-APR-1992 (first entry)
 XX Human macrophage inflammatory protein (MIP) 2 alpha.
 DE Inducible; secretory; inflammatory response; cytokine.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH Peptide 1..34
 FT /label= signal
 XX WO9200326-A.
 XX WO9200327-A.
 XX 09-JAN-1992.
 XX 24-JUN-1991; 91WO-US04478.
 XX 19-JUN-1991; 91US-0715195.
 XX 22-JUN-1990; 90US-0541898.
 XX (CHIR-) CHIRON CORP.
 XX Tekamp-Olson P, Gallegos CA;
 PI WPI; 1992-041518/05.
 DR N-PSDB; Q20613.
 DR Human macrophage inflammatory protein 2-alpha - useful in
 PT treating infections, cancer, myelopoietic dysfunction and auto:
 PT immune diseases
 XX Disclosure; Fig 2; 68pp; English.

The sequence was deduced from the DNA sequence obtd. by screening the U937 cDNA library prepd. from poly-A+ RNA from PMA treated and LPS stimulated cells, using as probe a fragment isolated from the mMIP-2 cDNA (see Q20612) encoding most of the mature mMIP-2 amino acid sequence. Two classes of human cDNA homologous to mMIP-2 were found designated alpha and beta. The alpha form reproduced here is claimed in WO9200327; the beta form (Q20614) is claimed in WO9200326. The alpha form is the more abundant of the two. The genes can be used to produce recombinant MIP proteins for use in wound healing, to modulate myelopoiesis and to induce adjuvant activity.
 See also R20588, R20590 and R20528-30.

XX Sequence 107 AA;
 SQ Query Match 100.0%; Score 379; DB 13; Length 107;
 Best Local Similarity 100.0%; Pred. No. 2.3e-38;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APLATELRCQCQLTQGLHKLNIQSVKSPGPHCAQTEVIATLKGKACLNPA5PMVK 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 35 aplatelrcqcqltqglhklniqsvkspgphcaqteviatlkgkaclnpaspmvk 94
 QY 61 KIIEKMLKNGKSN 73
 ||||||||||||||
 Db 95 kliekmlkngksn 107

RESULT 9
 R20529
 ID R20529 standard; Protein; 107 AA.
 XX AC R20529;
 XX 23-APR-1992 (first entry)
 DT

XX Human macrophage inflammatory protein (MIP) 2 alpha.
 DE Inducible; secretory; inflammatory response; cytokine.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH Peptide 1..34
 FT /label= signal
 XX WO9200326-A.
 XX WO9200327-A.
 XX 09-JAN-1992.
 XX 24-JUN-1991; 91WO-US04482.
 XX 19-JUN-1991; 91US-0715194.
 XX 22-JUN-1990; 90US-0541897.
 XX (CHIR-) CHIRON CORP.
 XX Tekamp-Olson P, Gallegos CA;
 PI WPI; 1992-041519/05.
 DR N-PSDB; Q20729
 DR Human macrophage inflammatory protein 2-alpha - useful in
 PT treating infections, cancer, myelopoietic dysfunction and auto:
 PT immune diseases
 XX Disclosure; Fig 2; 68pp; English.
 XX The sequence was deduced from the DNA sequence obtd. by screening the U937 cDNA library prepd. from poly-A+ RNA from PMA treated and LPS stimulated cells, using as probe a fragment isolated from the mMIP-2 cDNA (see Q20728) encoding most of the mature mMIP-2 amino acid sequence. Two classes of human cDNA homologous to mMIP-2 were found designated alpha and beta. The alpha form reproduced here is claimed in WO9200327; the beta form (Q20530) is claimed in WO9200326. The alpha form is the more abundant of the two. The genes can be used to produce recombinant MIP proteins for use in wound healing, to modulate myelopoiesis and to induce adjuvant activity.
 See also R20588, R20590 and R20528-30.

XX Sequence 107 AA;
 SQ Query Match 100.0%; Score 379; DB 13; Length 107;
 Best Local Similarity 100.0%; Pred. No. 2.3e-38;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APLATELRCQCQLTQGLHKLNIQSVKSPGPHCAQTEVIATLKGKACLNPA5PMVK 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 35 aplatelrcqcqltqglhklniqsvkspgphcaqteviatlkgkaclnpaspmvk 94
 QY 61 KIIEKMLKNGKSN 73
 ||||||||||||||
 Db 95 kliekmlkngksn 107

RESULT 10
 R23034
 ID R23034 standard; Protein; 107 AA.
 XX AC R23034;
 XX 26-OCT-1992 (first entry)
 DT Human Gro beta cytokine.
 XX

KW Cytokine; inflammatory response; MAD-2; cancer diagnosis;
 KW Colonic epithelial tumour cell.

XX Homo sapiens.

XX Key Location/Qualifiers
 XX Peptide 1..35

FT /label= leader
 FT /note= "putative"
 FT 36..107
 FT /label= Gro_beta

XX W09206196-A.

XX 16-APR-1992.

XX 24-SEP-1991; 91WO-US06936.

XX 28-SEP-1990; 90US-0590223.

XX (CETU) CETUS CORP.

XX (UYNC-) UNIV OF NORTH CAROLINA.

XX Haskill JS, Nitecki DE, Ralph P;

XX WPI; 1992-150882/18.

XX N-PSDB; Q24266.

XX Gro beta and Gro gamma inflammatory cytokine(s) - for use in

XX diagnosing colon cancer

XX Claim 12; Fig 1B; 46pp; English.

XX The cDNA clone coding for inflammatory cytokine Gro-beta was
 CC isolated from a mezerin- and calcium ionophore-stimulated leukocyte
 CC cDNA library. The amino acid sequence of Gro beta was deduced from
 CC the nucleotide sequence. The level of Gro beta in inflammatory
 CC response cells can be used as an indication of a test substance's
 CC inflammatory activity and to diagnose colon cancer.
 CC See also Q24267.

XX Sequence 107 AA;

Query Match 100.0%; Score 379; DB 13; Length 107;
 Best Local Similarity 100.0%; Pred. No. 2.3e-38;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APLATELRQCCLQTLOGIHLKNIQSVKSPGPHCAQTEVIATLKNGQKACLNPA SPVVK 60
 |||||
 35 aplatelrqcclqtlgqihlknigsvkspgphcaqteviatlkngqkaclnpaspvkv 94

QY 61 KIIEKMLKNGKSN 73

Db 95 kilekmlkngksn 107

RESULT 11

ID W96714 standard; Protein; 107 AA.

XX AC W96714;

XX 15-APR-1999 (first entry)

XX Growth related oncogene-beta (GRO-beta).

XX Growth related oncogene-beta; GRO-beta; CXC chemokine; metastasis;
 KW angiogenesis inhibitor; angiostasis inducer; tumour growth inhibition;
 KW haemangiomas; rheumatoid arthritis; atherosclerosis; meningioma;
 KW idiopathic pulmonary fibrosis; benign prostatic hypertrophy; psoriasis;
 KW vascular restenosis; arteriovenous malformation; neovascular glaucoma;
 KW angiofibroma; haemophilic joint; hypertrophic scar; Osler-Weber syndrome;

KW

KW pyogenic granuloma retrolental fibroplasia; scleroderma; trachoma;
 KW vascular adhesion; synovitis; dermatitis; endometriosis; pterygium;
 KW diabetic retinopathy; neovascularisation; chronic bronchitis;
 KW adult respiratory distress syndrome; ARDS; pseudogout;
 KW cystic fibrosis.

XX Homo sapiens.

XX US5871723-A.

XX 16-FEB-1999.

XX 06-JUN-1995; 95US-0468819.

XX 06-JUN-1995; 95US-0468819.

XX (UNMI) UNIV MICHIGAN.

XX Kunkel SL, Polverini PJ, Strieter RM;

XX WPI; 1999-166569/14.

XX N-PSDB; X15002.

XX Use of chemokines with a conserved Cys Xaa Cys (CXC) sequence -
 CC which do not contain amino acid sequence ELR, for inhibiting
 CC angiogenesis in tumours, rheumatoid arthritis, restenosis or
 CC glaucoma

XX Disclosure; Columns 95-96; 145pp; English.

XX The present sequence is a growth related oncogene-beta (GRO-beta).
 CC GRO-alpha is a CXC chemokine that is an inhibitor of angiogenesis.
 CC The specification describes methods for inhibiting angiogenesis or for
 CC inducing angiostasis, using chemokines (with a conserved Cys Xaa Cys
 CC (CXC) sequence at the N-terminal) other than platelet factor-4, and
 CC which do not contain the amino acid sequence ELR. The methods are useful
 CC for inhibiting tumour growth and metastasis and for treating diseases
 CC such as haemangiomas, rheumatoid arthritis, atherosclerosis and
 CC idiopathic pulmonary fibrosis (IPF), benign prostatic hypertrophy (BPH),
 CC vascular restenosis, arteriovenous malformations (AVM), meningioma,
 CC neovascular glaucoma, psoriasis, angiofibroma, haemophilic joints,
 CC hypertrophic scars, Osler-Weber syndrome, pyogenic granuloma retrolental
 CC fibroplasia, scleroderma, trachoma, vascular adhesions, synovitis,
 CC dermatitis, endometriosis, pterygium, diabetic retinopathy
 CC neovascularisation associated with corneal injury or grafts, adult
 CC respiratory distress syndrome (ARDS), chronic bronchitis, pseudogout
 CC and cystic fibrosis.

XX Sequence 107 AA;

Query Match 100.0%; Score 379; DB 20; Length 107;
 Best Local Similarity 100.0%; Pred. No. 2.3e-38;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APLATELRQCCLQTLOGIHLKNIQSVKSPGPHCAQTEVIATLKNGQKACLNPA SPVVK 60
 |||||
 35 aplatelrqcclqtlgqihlknigsvkspgphcaqteviatlkngqkaclnpaspvkv 94

QY 61 KIIEKMLKNGKSN 73

Db 95 kilekmlkngksn 107

RESULT 12

ID B15810 standard; Protein; 107 AA.

XX AC B15810;

XX 17-JAN-2001 (first entry)

XX Human chemokine GRObeta SEQ ID NO: 53.

XX Macrophage recruitment; chemokine derivative; MCP-1; osteoporosis;
 KW monocyte chemoattractant protein-1; inflammation; atherosclerosis; HIV;
 KW AIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxaemia;
 KW basophil-mediated disease; myocardial infarction; acute ischaemia;
 KW rheumatoid arthritis; contraception.

XX Homo sapiens.

XX WO200042071-A2.

XX 20-JUL-2000.

XX 12-JAN-2000; 2000WO-US00821.

XX 12-JAN-1999; 99US-0229071.

XX 17-MAR-1999; 99US-0271192.

XX 01-DEC-1999; 99US-0452406.

XX (NEOR-) NEORX CORP.

XX Grainger DJ, Tatalick LM;

XX WPI; 2000-499101/44.

XX DR N-PSDB; A74871.

XX New peptide 3, amide and heterocyclic compounds and saccharide
 PT conjugates used for inhibiting chemokine induced activity and for
 PT treating e.g. stroke, vascular diseases, autoimmune diseases and tumour
 PT growth -
 XX Disclosure; Page 364; 387pp; English.

XX The present invention concerns the identification of a number of
 CC chemokines which can be used to produce derivatives, agonists and
 CC antagonists which are then useful in disease treatment. The chemokines
 CC include sequences B15785-B15794, B15803-B15813 and B15831-B15848. These
 CC chemokine derivatives can be used to treat diseases such as autoimmune
 CC diseases, atherosclerosis, osteoporosis, HIV infection and AIDS,
 CC psoriasis, inflammatory diseases, hypertension, basophil-mediated
 CC diseases, endotoxaemia, myocardial infarction, acute ischaemia and
 CC rheumatoid arthritis, and can be used to prevent strokes and as
 CC contraceptives. The coding sequences for the chemokines can be used in
 CC gene therapy for the same diseases, as well as in the production of
 CC animal models.

XX Sequence 107 AA;

Query Match 100.0%; Score 379; DB 21; Length 107;
 Best Local Similarity 100.0%; Pred. No. 2.3e-38;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APLATELRCQCLOTLQGLHKLNIQSVKSPGPHCAOTEVIATLKGOKACLNPMVK 60

Db 35 aplatelrcqcltqlgihlniqsvkspgphcaqteviatlkgkaclnpasmvk 94

QY 61 KIIEKMLKNGKSN 73

Db 95 kiiekmlkngksn 107

RESULT 13

R70793

ID R70793 standard; Protein; 102 AA.

AC R70793;

DT 29-AUG-1995 (first entry)

DE Gro-beta/MIP-2-alpha.

XX Macrophage inflammatory protein 2-alpha; gro-beta/MIP-2-alpha;

KW heparanase; heparin; heparan sulfate; arthritis; restenosis;
 KW cancer; wound healing.

XX Homo sapiens.

XX WO9504158-A.

XX 09-FEB-1995.

XX 26-JUL-1994; 94WO-US08207.

XX 29-JUL-1993; 93US-0099866.

XX 13-OCT-1993; 93US-0136117.

XX (UPJO) UPJOHN CO.

XX Hoogwerf AJ, Ledbetter SR;

XX WPI; 1995-082239/11.

XX DR N-PSDB; Q85363.

XX Screening for cpds. with anti-heparanase activity - by detecting
 PT inhibition of heparin or heparan sulphate degradation,
 PT potentially useful for treating arthritis, restenosis, cancer.

XX Claim 12; Page 40; 60pp; English.

XX Purified heparanases, prepared under reducing conditions and
 CC activated with transglutaminase, are given in R70786-804. Most
 CC are prepared by reverse transcription of mRNA from activated human
 CC leukocytes, then cloning of the cDNA into pVL1392 baculovirus
 CC vector, and expression in Sf9 cells in the presence of reduced
 CC glutathione and dithiothreitol.

XX Sequence 102 AA;

Query Match 92.9%; Score 352; DB 16; Length 102;
 Best Local Similarity 100.0%; Pred. No. 3.9e-35;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APLATELRCQCLOTLQGLHKLNIQSVKSPGPHCAOTEVIATLKGOKACLNPMVK 60

Db 35 aplatelrcqcltqlgihlniqsvkspgphcaqteviatlkgkaclnpasmvk 94

QY 61 KIIEKMLK 68

Db 95 kiiekmlk 102

RESULT 14

R66698

ID R66698 standard; protein; 73 AA.

AC R66698;

DT 19-JUL-1995 (first entry)

DE Human gro-alpha chemokine..

XX Gro-alpha protein; chemokine; inflammation; antiinflammatory;
 KW hematopoietic synergistic factor; HSF; hematopoietic precursor;
 KW bone marrow; interleukin; desamino gro-alpha; truncation.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Protein 5..732

FT /note= "desamino truncated gro-alpha, claim 7,
 FT page 69"

XX WO9429341-A.

PD 22-DEC-1994.

XX- 03-JUN-1994; 94WO-US06264.

XX 08-JUN-1993; 93US-0073800.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Balcarek JM, Bhatnagar P, King AG, Pelus LM;

XX WPI; 1995-036402/05.

XX New truncated chemokine with increased biological activity - and
PT related multimers, nucleic acid, antibodies etc., for treating
PT inflammation, stimulating growth of bone marrow etc., also
PT peptide(s) for inducing haematopoietic synergistic factor.

XX Disclosure; Page 51; 89pp; English.

XX Truncated, desamino chemokine comprising amino acids 5-73 of
CC human mature gro-alpha (full sequence given in R66698)XX shows enhanced biological activity when compared to the mature
XX protein, and has been used to prepare multimeric, modified
XX chemokines.

XX SQ Sequence 73 AA;

Query Match 87.3%; Score 331; DB 16; Length 73;

Best Local Similarity 87.7%; Pred. No. 8.8e-33;

Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 APLATELRCQCLOTLQGIHLKNIQSVKSPGPHCAQTEVIATLKNQKACLNPMVK 60

Db 1 asvatelrcqccltqlgihpkniqsvnvksppghcaqteviatlkngkaclnpaspvk 60

QY 61 KIIEKMLKNGKSN 73

Db 61 kiiekmlnsdksn 73

RESULT 15

W18024

XX ID W18024 standard; protein; 73 AA.

XX AC W18024;

XX DT 30-JAN-1998 (first entry)

XX Human chemokine gro alpha.

XX Sepsis; septic shock; therapy; gro alpha; chemokine; human.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Protein 5..73

XX FT /note= "preferred modified fragment of KC

XX FT (Claim 4)"

XX PN W09719173-AL.

XX PD 29-MAY-1997.

XX PF 20-NOV-1996; 96WO-US18616.

XX PR 21-NOV-1995; 95US-0007425.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PI DeMarsh PL, Johanson KO;

XX DR WPI; 1997-298111/27.

*1

*2

XX

PT Use of chemokine(s) such as KC and gro-alpha - to treat or prevent
PT sepsis, particularly septic shock

XX Claim 1; Page 18-19; 28pp; English.

XX A claimed method of treating or preventing sepsis comprises
CC administering to an animal an effective amount of a chemokine
CC selected from mature murine KC (see W18023), human gro alpha
CC (W18024), human gro beta (see W18025) and human gro gamma (see
CC W18026), modified fragments of these chemokines and multimeric
CC proteins comprising an association of two chemokine proteins.CC Sepsis can occur in hospitalised patients, and a consequence of
CC bacterial sepsis is septic shock. The method of the invention
CC provides a treatment for sepsis, particularly septic shock, which
CC is a major cause of death in intensive care units. Septic shock
CC syndrome apparently has intractable resistance to the effects of
CC a variety of highly potent antimicrobial agents. Survival is
CC increased by treatment with the chemokines, both prophylactically
CC and after infection.

XX SQ Sequence 73 AA;

Query Match 87.3%; Score 331; DB 18; Length 73;

Best Local Similarity 87.7%; Pred. No. 8.8e-33;

Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 APLATELRCQCLOTLQGIHLKNIQSVKSPGPHCAQTEVIATLKNQKACLNPMVK 60

Db 1 asvatelrcqccltqlgihpkniqsvnvksppghcaqteviatlkngkaclnpaspvk 60

QY 61 KIIEKMLKNGKSN 73

Db 61 kiiekmlnsdksn 73

Search completed: May 4, 2001, 07:37:02

Job time: 94 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 4, 2001, 07:35:28 ; Search time 11.75 Seconds
(without alignments)
119.353 Million cell updates/sec

Title: US-09-467-160-3
Perfect score: 379
Sequence: 1 APLATELRCQQLTQGIHL.....PASPMVKIIEKMLKNGKSN 73

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pap.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pap.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pap.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pap.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pap.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	379	100.0	73	1	US-07-792-988-3
2	379	100.0	73	1	US-07-778-413E-19
3	379	100.0	73	1	US-08-340-102-20
4	379	100.0	73	2	US-08-436-420-27
5	379	100.0	73	3	US-08-846-966-3
6	379	100.0	73	3	US-08-557-142-3
7	379	100.0	73	5	PCT-US94-06264-3
8	379	100.0	107	1	US-08-352-324A-4
9	379	100.0	107	2	US-08-862-607-4
10	379	100.0	107	2	US-08-488-819-6
11	379	100.0	107	3	US-09-203-235-4
12	379	100.0	107	5	PCT-US95-16144-4
13	367	96.8	73	1	US-08-330-163-3
14	367	96.8	73	1	US-08-482-111-3
15	331	87.3	73	1	US-07-778-413E-18
16	331	87.3	73	1	US-08-340-102-18
17	331	87.3	73	1	US-08-330-163-2
18	331	87.3	73	1	US-08-482-111-2
19	331	87.3	73	2	US-08-436-420-26
20	331	87.3	73	3	US-08-846-966-2
21	331	87.3	73	3	US-08-557-142-2
22	331	87.3	73	5	PCT-US94-06264-2
23	331	87.3	107	1	US-08-352-324A-7
24	331	87.3	107	2	US-08-862-607-7
25	331	87.3	107	2	US-08-488-819-5
26	331	87.3	107	3	US-09-203-235-7
27	331	87.3	107	5	PCT-US95-16144-7

28	325	85.8	73	1	US-07-792-988-4	Sequence 4, Appl
29	325	85.8	73	1	US-07-778-413E-20	Sequence 20, Appl
30	325	85.8	73	1	US-08-340-102-20	Sequence 20, Appl
31	325	85.8	73	1	US-08-330-163-4	Sequence 4, Appl
32	325	85.8	73	1	US-08-482-111-4	Sequence 4, Appl
33	325	85.8	73	2	US-08-436-420-28	Sequence 28, Appl
34	325	85.8	73	3	US-08-846-966-4	Sequence 4, Appl
35	325	85.8	73	3	US-08-557-142-4	Sequence 4, Appl
36	325	85.8	73	5	PCT-US94-06264-4	Sequence 4, Appl
37	325	85.8	106	1	US-08-352-324A-5	Sequence 5, Appl
38	325	85.8	106	2	US-08-862-607-5	Sequence 5, Appl
39	325	85.8	106	2	US-08-488-819-7	Sequence 7, Appl
40	325	85.8	106	3	US-09-203-235-5	Sequence 5, Appl
41	325	85.8	106	5	PCT-US95-16144-5	Sequence 5, Appl
42	296	78.1	78	2	US-08-436-420-38	Sequence 38, Appl
43	284	74.9	72	2	US-08-436-420-39	Sequence 39, Appl
44	278	73.4	72	3	US-08-846-966-1	Sequence 1, Appl
45	278	73.4	72	3	US-08-557-142-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-07-792-988-3
; Sequence 3, Application US/07792988
; Patent No. 5306709
; GENERAL INFORMATION:
; APPLICANT: Gewirtz, Alan M.
; TITLE OF INVENTION: Suppression of megakaryo-
; TITLE OF INVENTION: cytopoiesis by macrophage inflammatory proteins
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: University of Pennsylvania
; STREET: Suite 419
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19104-3246
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/792,988
; FILING DATE: 19911115
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 6056-159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: No. 5306709e
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 73 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
US-07-792-988-3

Query Match 100.0%; Score 379; DB 1; Length 73;
Best Local Similarity 100.0%; Pred No. 1.7e-40;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 APLATELCQCLOTLQGIHLKNIQSVKSPGPHCAQTEVIATLKNQKACLNPA SPVK 60
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Db 1 APLATELCQCLOTLQGIHLKNIQSVKSPGPHCAQTEVIATLKNQKACLNPA SPVK 60
OY 61 KIIEKMLKNGKSN 73
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Db 61 KIIEKMLKNGKSN 73

RESULT 2

US-07-778-413E-19
; Sequence 19, Application US/07778413E
; Patent No. 5401651
; GENERAL INFORMATION:
; APPLICANT: Walz, Alfred
; TITLE OF INVENTION: No. 5401651el Neutrophil
; ACTIVATING FACTORS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehaviiland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 in., DS, 2.0 MB
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh OS 7.0
; SOFTWARE: Microsoft Word Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07778,413E
; FILING DATE: 16-OCT-1991
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Cook, Robert R.
; REGISTRATION NUMBER: 31602
; REFERENCE/DOCKET NUMBER: A-204
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (805) 499-8011
; TELEFAX: (805) 499-5725 EXTENSION 4955
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 73 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-778-413E-19

Query Match 100.0%; Score 379; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.7e-40;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 APLATELCQCLOTLQGIHLKNIQSVKSPGPHCAQTEVIATLKNQKACLNPA SPVK 60
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Db 1 APLATELCQCLOTLQGIHLKNIQSVKSPGPHCAQTEVIATLKNQKACLNPA SPVK 60
OY 61 KIIEKMLKNGKSN 73
|||||
Db 61 KIIEKMLKNGKSN 73

RESULT 3

US-08-340-102-19
; Sequence 19, Application US/08340102
; Patent No. 5591718
; GENERAL INFORMATION:
; APPLICANT: Walz, Alfred
; TITLE OF INVENTION: No. 5591718el Neutrophil
; ACTIVATING FACTORS
; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehaviiland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 in., DS, 1.4 MB
; COMPUTER: MS-DOS
; OPERATING SYSTEM: MS-DOS 6.22
; SOFTWARE: Microsoft Word Version 5.1a for
; SOFTWARE: Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,102
; FILING DATE: 15-NOV-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Cook, Robert R.
; REGISTRATION NUMBER: 31602
; REFERENCE/DOCKET NUMBER: A-204A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (805) 499-8011
; TELEFAX: (805) 499-5725 EXTENSION 4955
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 73 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-340-102-19

Query Match 100.0%; Score 379; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.7e-40;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 APLATELCQCLOTLQGIHLKNIQSVKSPGPHCAQTEVIATLKNQKACLNPA SPVK 60
OY 61 KIIEKMLKNGKSN 73
|||||
Db 61 KIIEKMLKNGKSN 73

RESULT 4

US-08-436-420-27
; Sequence 27, Application US/08436420
; Patent No. 5840524

; GENERAL INFORMATION:
; APPLICANT: VAN DAMME, Jo; and
; APPLICANT: PROOST, Paul
; TITLE OF INVENTION: GRANULOCYTE CHEMOTACTIC PROTEIN
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE and DORR LLP
; STREET: 1455 PENNSYLVANIA AVENUE, N.W.
; CITY: WASHINGTON
; STATE: DISTRICT OF COLUMBIA
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,420
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/03330
FILING DATE: 26-NOV-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/982,539
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 102378.215
TELEPHONE: (202) 942-8400
TELEFAX: (202) 942-8484
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 73 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-436-420-27

Query Match 100.0%; Score 379; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.7e-40;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 APLATELCQCLOTLQGHILKNIQSVKSPGPHCAQTEVIATLKGQKACLNPAWPK 60
QY 61 KIIEKMLKNGKSN 73
Db 61 KIIEKMLKNGKSN 73

RESULT 5
US-08-846-966-3
Sequence 3, Application US/08846966
Patent No. 6042821
GENERAL INFORMATION:
APPLICANT: SmithKline Beecham Corporation
APPLICANT: Demarsh, Peter L.
APPLICANT: Johanson, Kyung O.
TITLE OF INVENTION: Method of Treating Sepsis
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation - Corporate Patents
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846.966
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/007,425
FILING DATE: 21-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hall, Linda E.
REGISTRATION NUMBER: 31,763
REFERENCE/DOCKET NUMBER: P50417-1
TELEPHONE: 610-270-5016
TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 73 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-846-966-3

Query Match 100.0%; Score 379; DB 3; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.7e-40;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 APLATELCQCLOTLQGHILKNIQSVKSPGPHCAQTEVIATLKGQKACLNPAWPK 60
QY 61 KIIEKMLKNGKSN 73
Db 61 KIIEKMLKNGKSN 73

RESULT 6
US-08-557-142-3
Sequence 3, Application US/08557142
Patent No. 6080398
GENERAL INFORMATION:
APPLICANT: Pelus, Louis M
APPLICANT: Bhatnagar, Pradip K
APPLICANT: King, Andrew G
APPLICANT: Balcarek, Joanna M
TITLE OF INVENTION: Methods of Enhancing Bioactivity of
TITLE OF INVENTION: Chemokines
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation -
ADDRESSEE: Corporate Patents
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,142
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,800
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hall, Linda E.
REGISTRATION NUMBER: 31,763
REFERENCE/DOCKET NUMBER: SBCEP50161
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-270-5015
TELEFAX: 215-270-5090
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 73 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-557-142-3

Query Match 100.0%; Score 379; DB 3; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.7e-40;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
US-08-352-324A-4
; Sequence 4, Application US/08352324A
; Patent No. 5633149
; GENERAL INFORMATION:
; APPLICANT: Guegler, Karl J.

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RESULT          9
US-08-862-607-4
; Sequence 4, Application US/08862607
; Patent NO. 5844084
; GENERAL INFORMATION:
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Wilde, Craig G.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: A NOVEL CHEMOKINE EXPRESSED IN
; TITLE OF INVENTION: INFLAMED ADENOID, ITS PRODUCTION AND USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

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	Query Match	100.0%;	Score 379;	DB 2;	Length 107;
	Best Local Similarity	100.0%;	Pred. No. 2.7e-40;		
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Db	35	APLATELRCCQLTQLOGIHLKNIQSVKVSPPGHCQAQTEVIATLKNQCKACLNPASPMVK	94		
QY	61	KIIEKMLKNGKSN	73		
Db	95	KIIEKMLKNGKSN	107		

US-09-203-233-4
; Sequence 4, Application US/09203235
; Patent No. 6071701
; GENERAL INFORMATION:

/ REFERENCE: Gueyria, Raymond
 / APPLICANT: Hawkins, Phillip R.
 / APPLICANT: Wilde, Craig G.
 / APPLICANT: Seilhamer, Jeffrey J.
 / TITLE OF INVENTION: A NOVEL CHEMOKINE EXPRESSED IN
 / TITLE OF INVENTION: INFLAMED ADENOID, ITS PRODUCTION AND USES
 / NUMBER OF SEQUENCES: 9
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Incyte Pharmaceuticals, Inc.

SIRIEL: 3174 POLICE DRIVE
CITY: Palo Alto .
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/203,235
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/862,607
FILING DATE: 23-MAY-1997
APPLICATION NUMBER: 08/352,324
FILING DATE: 07-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0025 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-203-235-4

US-09-203-235-4

RESULT 13

; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30B
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/482,111
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fasse, J. Peter
 ; REGISTRATION NUMBER: 32,983
 ; REFERENCE/DOCKET NUMBER: 00231/083001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 542-5070
 ; TELEFAX: (617) 542-8906
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 73 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-482-111-3

Query Match 96.8%; Score 367; DB 1; Length 73;
 Best Local Similarity 97.3%; Pred. No. 5.4e-39;
 Matches 71; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 APLATELCQCLOTLOGIHLKNIQSVKSPGPHCAQTEVIATLKNGOKACLNPPASPMVK 60
 Db 1 APLATELCQCLOTLOGIHLKNIQSVKSPGPHCAQTEVIATLKNGOKACLNPPASPMVK 60
 Qy 61 KIIEKMLKNGKSN 73
 Db 61 KIIEKMLKNGKSN 73

RESULT 15
 US-07-778-413E-18
 ; Sequence 18, Application US/07778413E
 ; Patent No. 5401651
 ; GENERAL INFORMATION:
 ; APPLICANT: Walz, Alfred
 ; TITLE OF INVENTION: No. 5401651el Neutrophil
 ; TITLE OF INVENTION: Activating Factors
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Amgen Inc.
 ; STREET: Amgen Center
 ; STREET: 1840 Dehavenland Drive
 ; CITY: Thousand Oaks
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 91320-1789
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.5 in., DS, 2.0 MB
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Macintosh OS 7.0
 ; SOFTWARE: Microsoft Word Version 5.1a
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/778,413E
 ; FILING DATE: 16-OCT-1991
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Cook, Robert R.
 ; REGISTRATION NUMBER: 31602
 ; REFERENCE/DOCKET NUMBER: A-204
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (805) 499-5725 EXTENSION 4955
 ; TELEFAX: (805) 499-8011
 ; INFORMATION FOR SEQ ID NO: 18:
 ; SEQUENCE CHARACTERISTICS:

; LENGTH: 73 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-07-778-413E-18
 Query Match 87.3%; Score 331; DB 1; Length 73;
 Best Local Similarity 87.7%; Pred. No. 1.7e-34;
 Matches 64; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 APLATELCQCLOTLOGIHLKNIQSVKSPGPHCAQTEVIATLKNGOKACLNPPASPMVK 60
 Db 1 ASVATELCQCLOTLOGIHLKNIQSVKSPGPHCAQTEVIATLKNGOKACLNPPASPIVK 60
 Qy 61 KIIEKMLKNGKSN 73
 Db 61 KIIEKMLNSDKSN 73
 Search completed: May 4, 2001, 07:36:40
 Job time: 72 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run On: May 4, 2001, 07:35:28 ; Search time 14.16 seconds
(without alignments)
354.292 Million cell updates/sec

Title: US-09-467-160-3
Perfect score: 379
Sequence: 1 APLATELRCCLOTLQLOGIHL.....PASPMVKKIETKMLKNGKSN 73

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Search: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_67.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	379	100.0	107	JH0281	macrophage inflamm
2	331	87.3	107	A28414	melanoma growth-st
3	325	85.8	107	B38290	GRO-gamma precuso
4	304	80.2	101	B28414	growth-regulated p
5	284	74.9	96	JN0572	neutrophil chemo-a
6	278	73.4	96	A32954	gro-alpha precuso
7	261	68.9	100	JH0200	macrophage inflamm
8	249	65.7	100	S21467	macrophage inflamm
9	249	65.7	100	I5614	macrophage inflamm
10	233	61.5	100	A46198	cytokine-induced n
11	212	55.9	53	I64831	gene KC protein -
12	210	55.4	117	B42583	macrophage inflamm
13	210	55.4	119	A24881	platelet basic pro
14	209	55.1	128	1 TGHU	beta-thromboglobul
15	208	54.9	75	B34188	granulocyte chemot
16	199.5	52.6	114	A55010	neutrophil-activat
17	178	47.0	53	I31886	macrophage inflamm
18	176.5	46.6	103	A26736	transformation-ind
19	176.5	46.6	103	I50417	RSV-induced protei
20	173	45.6	75	A54188	granulocyte chemot
21	173	45.6	90	S69133	platelet factor 4
22	168	44.3	125	JN0470	interferon gamma-1
23	166.5	43.9	105	A26774	platelet factor 4
24	166	43.8	36	S17507	cytokine - rabbit
25	164.5	43.4	99	A37034	interleukin-8 prec
26	163	43.0	132	A57325	C-X-C chemokine LI
27	160	42.2	101	1 PFHU4	platelet factor 4
28	160	42.2	126	A35766	platelet factor 4
29	155.5	41.0	101	2 S42496	interleukin 8 - sh

30	155.5	41.0	101	2	I46997	interleukin-8 - sh
31	151	39.8	33	2	S50035	cytokine bGRO - b
32	151	39.8	88	1	PFBO4	platelet factor 4
33	150.5	39.7	101	2	I46871	interleukin-8 - ra
34	146.5	38.7	103	2	A44253	alveolar macrophag
35	146.5	38.7	103	2	A53096	interleukin-8 prec
36	145.5	38.4	95	2	JN0841	interleukin-8 - do
37	142	37.5	104	1	PFHU4A	platelet factor 4
38	130.5	34.4	101	2	I48148	Neutrophil attract
39	113	29.8	98	1	TGHUGI	interferon gamma-i
40	107	28.2	40	2	S33290	lipopolysaccharide
41	105	27.7	98	2	A45492	IP-10 precursor -
42	105	27.7	98	2	I59277	Mob-1 - rat
43	87.5	23.1	99	2	JG0182	chemokine BRAK - h
44	81.5	21.5	89	2	A53497	pre-B-cell growth-
45	81.5	21.5	89	2	I53416	interleukin-8 homo

ALIGNMENTS

RESULT 1

JH0281

macrophage inflammatory protein 2 alpha precursor - human

N:Alternate names: gro-beta; growth regulated protein beta; melanoma growth-stimulat

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 20-Aug-1999

C:Accession: JH0281; A35931; A38290; A60407

R:Tekamp-Olson, P.; Gallegos, C.; Bauer, D.; McClain, J.; Sherry, B.; Fabre, M.; van

J. Exp. Med. 172, 911-919, 1990

A:Title: Cloning and characterization of cDNAs for murine macrophage inflammatory pro

A:Reference number: JH0200; MUID:90354792

A:Accession: JH0281

A:Molecule type: mRNA

A:Residues: 1-107 <TEK>

A:CROSS-references: GB:X53799; NID:g34658; PIDN:CAA37808.1; PID:g34659

R:Tida, N.; Grotendorst, G.R.

Mol. Cell. Biol. 10, 5596-5599, 1990

A:Title: Cloning and sequencing of a new gro transcript from activated human monocyte

A:Reference number: A35931; MUID:90377259

A:Accession: A35931

A:Molecule type: mRNA

A:Residues: 1-107 <IID>

A:CROSS-references: GB:M57731; GB:M36964; NID:g183626; PIDN:AAA63182.1; PID:g183627

R:Haskill, S.; Peace, A.; Morris, J.; Sporn, S.A.; Anisowicz, A.; Lee, S.W.; Smith, T

Proc. Natl. Acad. Sci. U.S.A. 87, 7732-7736, 1990

A:Title: Identification of three related human GRO genes encoding cytokine functions.

A:Reference number: A38290; MUID:91017578

A:Accession: A38290

A:Molecule type: mRNA

A:Residues: 1-107 <HAS>

A:CROSS-references: GB:M36820; NID:g183628; PIDN:AAA63183.1; PID:g183629

R:Sporn, S.A.; Elerman, D.F.; Johnson, C.E.; Morris, J.; Martin, G.; Ladner, M.; Hask

J. Immunol. 144, 4434-4441, 1990

A:Title: Monocyte adherence results in selective induction of novel genes sharing hom

A:Reference number: A60407; MUID:90257367

A:Accession: A60407

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 56-107 <SPO>

C:Superfamily: beta-thromboglobulin

C:Keywords: Inflammation

F:1-34/Domain: signal sequence #status predicted <SIG>

F:35-107/Product: macrophage inflammatory protein 2 alpha #status predicted <NAT>

Query Match 100.0%; Score 379; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e-35;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APLATELRCCLOTLQLOGIHLKNIQSVKSPGPHCAQTEVIATLKNGOKACLNPA5PMVK 60
DB 35 APLATELRCCLOTLQLOGIHLKNIQSVKSPGPHCAQTEVIATLKNGOKACLNPA5PMVK 94

A/Cross-references: GDB:120181; OMIM:155730

A:Status: preliminary
A:Molecule type: protein
A:Residues: 25-57 <NA2>
A:Experimental source: kidney, NRX-49F fibroblasts
A:Note: sequence extracted from NCBI backbone (NCBIP:129131)
R:Hanzawa, H.; Haruyama, H.; Watanabe, K.; Tsurufuji, S.
FEBS Lett. 354, 207-212, 1994

A:Reference number: S51214; MOL_ID: S51214
A:Contents: annotation; conformation by (1)H-NMR, residues 25-96
A:Accession: S51214
A:Molecule type: protein
A:Residues: 25-96 <HAN>
C:Comment: This protein has chemotactic activity for neutrophils and has melanoma growth-inhibitory activity
C:Genetics:

A: introns: 24/11; 03/21; 54/2
C: Superfamily: beta-thromboglobulin
C: Keywords: cytokine; disulfide bond
F: 1-24/Domain: signal sequence #status
predicted <SIG>

Query Match	Score 284;	DB 2;	Length 96;
74.9%			

Matches 51: **Conservative** 10: **Mismatches** 7:
Best local similarity 75.00; **PID: N:** 5.1E-25;
Gaps 0: Gaps 0;

0v 1 APLATELRCCOCLOTLOGIHLKNIOSVKVKSPPGPHCAOTEVIATLKNKGOKACLNPASPMPVK 60

DB 25 APVANE LRCQ C D Q T V A G I H F R N I Q S L K V M P P G P F H C T Q T E V I A I L K N G R E A C L D F E A F M V Q 84

QY 01 KILKMLA 00
||::|||
Db 85 KIVQMLK 92

RESULT 6
A32954
gro-alpha precursor - mouse
N:Alternate names: gro protein; growth regulated protein; melanoma growth-stimulating

C>Date: 20-Oct-1989 #sequence_revision 20-Oct-1989 #text_change 20-Aug-1989
C/Accession: A32954; JH0081
R/Quoyendo, P.; Alberta, J.; Wen, D.; Graycar, J.L.; Derynck, R.; Stiles, C.D.
J. Biol. Chem. 264, 4133-4137, 1989
A/Title: The platelet-derived growth factor-inducible KC gene encodes a secretory protein
A/Reference number: A32954; MUID:89139485
A/Accession: A32954
A/Molecule type: mRNA

A:Cross-references: GB:J04296; NID:g20104; PID:AAAA0131.1; PID:g201043
R:Ryseck, R.P.; MacDonald-Bravo, H.; Mattei, M.G.; Bravo, R.
Exp. Cell Res. 180, 266-275, 1989
A:Title: Cloning and sequence of a secretory protein induced by growth factors in mouse
A:Reference number: JH0081; MUID:89078502
A:Accession: JH0081
A:Molecule type: mRNA
A:Residues: 1-96 <RYS>
C:Comment: This protein is basic and lacks threonine, phenylalanine and tyrosine

C:Genetics:
A:Map position: 5
C:Superfamily: beta-thromboglobulin
C:Keywords: extracellular protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-96/Product: gro-alpha #status predicted <MAT>

QY 1 APLATELRCCOCLQTLOGIHLKNIOSVKVSPGPHCAQTEVIATLKNGQKACLNPASPMVK 60
 ||| : ||||| |::||| : ||||| |::||| : ||||| |::||| : |||
Best Local Similarity 73.5%; **Pred. No.** 2.6e-24;
Matches 50; **Conservative** 11; **Mismatches** 7; **Indels** 0; **Gaps** 0;

Db 25 APIANELRCQLQTMAGIHLKNIQSLKVLPSGPHCTQTETIATLKNGREACLDPEAPLVQ 84

Qy 61 K I I E K M L K 68
Dy 85 K I V O K M L K 92

RESULT 7

AL3001 /
JH0200
macrophage inflammatory protein 2 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 20-Aug-1999
C:Accession: JH0200; A32190
R:Tekamp-Olson, P.; Gallegos, C.; Bauer, D.; McClain, J.; Sherry, B.; Fabre, M.; van De
J. Exp. Med. 172, 911-919, 1990
A:Title: Cloning and Characterization of cDNAs for murine macrophage inflammatory protein
A:Reference number: JH0200; MUID:903354792

A:Accession: JH0200
A:Molecule type: mRNA
A:Residues: 1-100 <TEK>
A:Cross-references: GB:X53128; NID:g53128; PID:g53129
Wolpe, S.D.; Sherry, B.; Juers, D.; Davatelis, G.; Yurt, R.W.; Cerami, A.
Proc. Natl. Acad. Sci. U.S.A. 86, 612-616, 1989
A:Title: Identification and characterization of macrophage inflammatory protein 2.
A:Reference number: A32190; MUID:89098980
A:Accession: A32190
A:Molecule type: protein
A:Residues: 28-59 <WOL>
A:Superfamily: beta-thromboglobulin
C:Keywords: heparin binding
F:1-27/Domain: signal sequence
F:28-100/Product: macrophage inflammatory protein 2 #status experimental <MAT>

Query Match	68.9%	Score 261;	DB 2;	Length 100;
Best Local Similarity	65.8%;	Pred. No. 2.2e-22;		
Matches 48;	Conservative 12;	Mismatches 13;	Indels 0;	Gaps 0;

Qy 1 APLATELCQCITLQIHLKNIQSVKVGPHCAQTEVIATLKNGQKACLNPASPMVK 60
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
D8 28 AVVASELCRCCLKTLPVRDFKNIQSLSVTPPGPHCAQTEVIATLKGGQKVCLDPEAPLVQ 87

Qy	61	KIIEKMLKNGSN	73
		: :	:
D _b	88	KIIOKILNKGKAN	100

RESULT
S21467
8

52140/ macrophage inflammatory protein 2 - rat
 Alternate names: chemoattractant p-1
 Species: Rattus norvegicus (Norway rat)
 C: Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Aug-1999
 C: Accession: S21467; D48988
 R: Driscoll, K.

K, DISCOLL, K.
submitted to the EMBL Data Library, April 1992

A:Reference number: S21467
A:Accession: S21467
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-100 <DRI>
A:Cross-references: EMBL:X65647; NID:X56665; PIDN:CAA46599.1; PID:X56666
R:Nakaogawa, H.; Ikesue, A.; Hatakeyama, S.; Kato, H.; Gotoda, T.; Komori
Biochem. Pharmacol. 45, 1425-1430, 1993
A:Title: Production of an interleukin-8-like chemokine by cytokine-stimu
A:Reference number: A48988; MUID:93228656
A:Accession: D48988

A;Status: preliminary
A;Molecule type: protein
A;Residues: 32-45 <NAK>
A;Experimental source: kidney, NRK-49F fibroblasts
A;Note: sequence extracted from NCBI backbone (NCBIP:129129)
C;Superfamily: beta-thromboqlobulin

Query Match 65.7%; Score 249; DB 2; Length 100;
Best Local Similarity 62.0%; Pred. No. 4.8e-21;
Matches 44; Conservative 14; Mismatches 13; Indels

QY **3** LATELRQCLOTLQGIHLKNIQSVKVSPGPHCAQTEVIATLKNGQACLNPA62
 :|:|:|:| : |:|:|:| : |:|:|:| :

D8 **30** VASELRQCCLTLPVRDFKNIQSLVTVPGPBHCQAETVIATKDGEHVCVLNPEAPLVQR89

QY	63	IEKMLKNGKSN	73
		: : : : :	
D _b	90	VQKILNKGN	100

RESULT 9

RESOLIN 3
I55614
macrophage inflammatory protein-2 - rat

macrophage inflammatory protein 2 rat
C/Species: Rattus sp. (rat)

C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996
C;Accession: I55614

R; Feng, L.; Xia, Y.; Yoshimura, T.; Wilson, C.B. J. Clin. Invest. 95, 1009-1017, 1995

A: Title: Modulation of neutrophil influx in glomerulonephritis in the rat with anti-m
A: Reference number: I55614; MUID:95189993

A;Accession: I55614
A;Status: preliminary; translated from GB/EMBL/DBJ

A; Molecule type: mRNA

A; Residues: 1-100 <RES>
A; Cross-references: GB:S77604; NID:g998406; PIDN:AAB33749.1; PID:g998407

Query Match 65.7%; Score 249; DB 2; Length 100;
Best Local Similarity 62.0%; Pred. No. 4.8e-21;
Matches 44; Conservative 14; Mismatches 13; Indels

QY

3 LATELRQCQLQTLOGIHUKNIQSVKVKSPGPHCAQTEVIATLKNQGKACLNPASPMVKKI 62
 :
dB

30 VASELRCCOLTLPRVDFEKNIQSITVTTPGPHCAQTEVIATLKDGHEVCNLPAPLVORI 89

Qy	63	IEKMLKNGKSN	73
		: : :	11 : 1
Db	90	VOKILNKGKAN	10

RESULT 10

S46198
cytokine-induced neutrophil chemoattractant 2 - rat
C; Species: Rattus norvegicus (Norway rat)

C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C; Accession: S46198; C48988
R; Nakagawa, H.; Komorita, N.; Shibata, F.; Ikesue, A.; Konishi, K.; Fujioaka,
Biochem. J. 301, 545-550, 1994
A; Title: Identification of cytokine-induced neutrophil chemoattractants (CIN)
ences and characterization.

A; Reference number: S46198; MUID: 94318061

A;Accession: S46198

A; Status: preliminary

A;Molecule type: mRNA

A;Residues: I-100 <NAK>
A;Cross-references: EMBL:D21095; NID:g517143; PIDN:BAA04657.1; PID:g517144

Biochem. Pharmacol. 45, 1425-1430, 1993
R.Nakagawa, H.; Ikesue, A.; Hatakeyama, S.; Kato, H.; Gotoda, T.; Komorita, N.; Watanabe, T. Production of an interleukin-8-like chemokine by autologous stimulated rat monocytes.

A;Title: Production of an interleukin-8-
 A;Reference number: M99989: MIMD-932298656

A; Reference number: A
A: Accession: C48988

A; Accession: C48308
A: Status: preliminary

A; Molecule type: protein

A; Residues: 33-56 <NA2>

A; Experimental source: kidney, NRK-49F fibroblasts

A;Note: sequence extracted from NCB
C;Superfamily: beta-thromboglobulin

R:Castor, C.W.; Miller, J.W.; Walz, D.A.
Proc. Natl. Acad. Sci. U.S.A. 80, 765-769, 1983
A:Title: Structural and biological characteristics of connective tissue activating peptide
A:Reference number: A93982; MUID:83144010
A:Accession: A93982
A:Molecule type: protein
A:Residues: 44-66;125-128 <CAS>
R:Beeg, G.S.; Pepper, D.S.; Chesterman, C.N.; Morgan, F.J.
Biochemistry 17, 1739-1744, 1978
A:Title: Complete covalent structure of human beta-thromboglobulin.
A:Reference number: A90411; MUID:78187279
A:Accession: A90411
A:Molecule type: protein
A:Residues: 48-128 <BEG>
R:Baeza, M.L.; Reddigari, S.R.; Kornfeld, D.; Ramani, N.; Smith, E.M.; Hossler, P.A.; F.
J. Clin. Invest. 85, 1516-1521, 1990
A:Title: Relationship of one form of human histamine-releasing factor to connective tiss
A:Reference number: A60709; MUID:90237229
A:Accession: A60709
A:Molecule type: protein
A:Residues: 44-62, 'X', 64-79 <BAE>
R:Kaplan, A.P.; Baeza, M.; Reddigari, S.; Kuna, P.
J. Arch. Allergy Appl. Immunol. 94, 148-153, 1991
A:Title: Histamine-releasing factors.
A:Reference number: A61240; MUID:92040226
A:Accession: A61240
A:Molecule type: protein
A:Residues: 44-61, 'XX', 64 <KAP>
A:Accession: B61240
A:Molecule type: protein
A:Residues: 59-62, 'X', 64-79 <KA2>
R:Kungl, A.J.; Machius, M.; Huber, R.; Schwer, C.; Lam, C.; Aschauer, H.; Ehn, G.; Lind
FEBS Lett. 347, 300-303, 1994
A:Title: Purification, crystallization and preliminary X-ray diffraction analysis of rec
A:Reference number: S46247; MUID:94307404
A:Contents: annotation
C:Comment: There appears to be a second beta-thromboglobulin-like human gene.
C:Comment: Connective-tissue activating peptides (CTAP) are a group of proteins capable
latelet, and polymorphonuclear leukocyte origin, respectively.
C:Comment: CTAP-III, a monomer isolated from platelets, stimulates DNA synthesis, mitosi
d sulfated glycosaminoglycan. It also stimulates the formation and secretion of plasmin
C:Comment: Proteolytic removal of the first four residues of CTAP-III produces the activ
ved growth factor.
C:Genetics:
A:Gene: GDB:PPBP; THBGBl
A:Cross-References: GDB:127391; OMIM:121010
A:Map position: 4p12-4q13
A:Introns: 50/1; 95/2
C:Superfamily: beta-thromboglobulin
Keywords: growth factor; homotetramer; platelet
-34/Domain: signal sequence #status predicted <SIG>
-35-43/Domain: propeptide #status predicted <PRO>
F:44-128/Product: connective-tissue activating peptide III #status experimental <CTAP>
F:48-128/Product: beta-thromboglobulin #status experimental <BTG>
F:59-128/Product: neutrophil-activating peptide 2 #status experimental <NAP2>
F:63-89,65-105/Disulfide bonds: #status experimental

Query Match 55.1%; Score 209; DB 1; Length 128;
Best Local Similarity 55.7%; Pred. No. 1.9e-16;
Matches 39; Conservative 12; Mismatches 19; Indels 0; Gaps 0;
QY 3 LATELCOCLOTLOGIHLKNIQSVKSPGPHCAQTEVIATLKGOKACLNPAASPVMVKI 62
| |||||:|:| |||||:|:| || || |||||:|:| ||:|:|:|:|
Db 57 LYAELRCMCITTSGLHPKNIQSVLEIVGKTHCNQVEVIATLKGDKRICLDPPAPRIKKI 116
QY 63 IEKMLKNGKS 72
:|:|:|:|
Db 117 VQKLAGDES 126

RESULT 15
B54188

granulocyte chemotactic protein, GCP-2 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 13-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 12-Apr-1995
R:Proost, P.; Wuyts, A.; Conings, R.; Lenaerts, J.P.; Billiau, A.; Opdenakker, G.; Va
Biochemistry 32, 10170-10177, 1993
A:Title: Human and bovine granulocyte chemotactic protein-2: complete amino acid sequ
A:Reference number: A54188; MUID:94001982
A:Accession: B54188
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-75 <PRO>
A:Experimental source: MDBK cells
A:Note: sequence extracted from NCBI backbone (NCBIP:137967)
C:Superfamily: beta-thromboglobulin
Query Match 54.9%; Score 208; DB 2; Length 75;
Best Local Similarity 50.0%; Pred. No. 1.4e-16;
Matches 36; Conservative 18; Mismatches 18; Indels 0; Gaps 0;
QY 1 APLATELCOCLOTLOGIHLKNIQSVKSPGPHCAQTEVIATLKGOKACLNPAASPVMVK 60
|:|:|:|:|:| |||||:|:| ||:|:|:|:|:| |||||:|:| ||:|:|:|:|
Db 4 AAVVRELRCVCLTPTPGIHPKTVSDLQVIAAGPQCSKVEVIATLKGREVCLDPEAPLIK 63
QY 61 KIEKMLKNGKS 72
||:|:|:|:|
Db 64 KIVQKILDSDGKN 75
Search completed: May 4, 2001, 07:36:24
Job time: 56 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 4, 2001, 07:35:28 ; Search time 9.61 Seconds
(without alignments)
260.213 Million cell updates/sec

Title: US-09-467-160-3

Perfect score: 379

Sequence: 1 APLATELRQCQLTQGIHL.....PASPVMVKIIFERMLKNGKSN 73

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	379	100.0	107	1	M12A_HUMAN
2	331	87.3	107	1	GRO_HUMAN
3	325	85.8	107	1	M12B_HUMAN
4	304	80.2	101	1	GRO_CRIGR
5	304	80.2	103	1	GRO_SHEEP
6	300	79.2	98	1	GROG_BOVIN
7	299	78.9	104	1	GROA_BOVIN
8	299	78.9	104	1	GROB_BOVIN
9	296	78.1	71	1	GROL_RABIT
10	295	77.8	104	1	GRO2_RABIT
11	284	74.9	96	1	GRO_RAT
12	278	73.4	96	1	GRO_MOUSE
13	261	68.9	100	1	MIP2_MOUSE
14	257	67.8	104	1	GRO_CAVPO
15	249	65.7	100	1	MIP2_RAT
16	237	62.5	68	1	M12A_RAT
17	233	61.5	100	1	M12B_RAT
18	210	55.4	117	1	AMC2_PIG
19	210	55.4	119	1	PF4L_PIG
20	209	55.1	128	1	PF4L_HUMAN
21	208	54.9	75	1	SZ06_BOVIN
22	199.5	52.6	114	1	SZ05_HUMAN
23	176.5	46.6	103	1	EMF1_CHICK
24	174	45.9	114	1	SZ06_HUMAN
25	173	45.6	85	1	PLF4_SHEEP
26	173	45.6	90	1	PLF4_PIG
27	168	44.3	125	1	SZ09_HUMAN
28	166.5	43.9	101	1	IL8_MACMU
29	166.5	43.9	105	1	PLF4_RAT
30	164.5	43.4	99	1	IL8_HUMAN
31	164.5	43.4	101	1	IL8_CERTO
32	163	43.0	132	1	SZ05_MOUSE
33	162.5	42.9	130	1	SZ05_RAT

34 160 42.2 101 1 PLF4_HUMAN P02776 homo sapien
35 160 42.2 126 1 SZ09_MOUSE P18340 mus musculus
36 155.5 41.0 101 1 IL8_BOVIN P79255 bos taurus
37 155.5 41.0 101 1 IL8_SHEEP P36925 ovis aries
38 151 39.8 88 1 PLF4_BOVIN P02777 bos taurus
39 150.5 39.7 101 1 IL8_RABIT P19874 oryctolagus
40 146.5 38.7 101 1 IL8_CANFA P41324 canis famil
41 146.5 38.7 103 1 IL8_PIG P26894 sus scrofa
42 142 37.5 104 1 PLFV_HUMAN P10720 homo sapien
43 138.5 36.5 97 1 IL8_HORSE O62812 equus cabal
44 130.5 34.4 101 1 IL8_CAVPO P49113 cavia porce
45 113 29.8 98 1 SZ10_HUMAN P02778 homo sapien

ALIGNMENTS

RESULT 1
ID M12A_HUMAN STANDARD; PRT; 107 AA.
AC P19875; Q9UPB8;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE MACROPHAGE INFLAMMATORY PROTEIN-2-ALPHA PRECURSOR (MIP2-ALPHA) (GROWTH
DE REGULATED PROTEIN BETA) (GRO-BETA).
GN GRO2 OR GROB OR MIP2A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Histocytic lymphoma;
RX MEDLINE=90354792; PubMed=2201751;
RA Tekamp-Olson P., Gallegos C., Bauer D., McClain J., Sherry B.,
RA Fabre M., van Deventer S., Cerami A.;
RT "Cloning and characterization of cDNAs for murine macrophage
RT inflammatory protein 2 and its human homologues.";
RL J. Exp. Med. 172:911-919(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90377259; PubMed=2078213;
RA Iida N., Grotendorst G.R.;
RT "Cloning and sequencing of a new gro transcript from activated human
RT monocytes: expression in leukocytes and wound tissue.";
RL Mol. Cell. Biol. 10:5596-5599(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=91017578; PubMed=2217207;
RA Haskill S., Peace A., Morris J., Sporn S.A., Anisowicz A., Lee S.W.,
RA Smith T., Martin G., Ralph P., Sager R.;
RT "Identification of three related human GRO genes encoding cytokine
RT functions.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:7732-7736(1990).
RN [4]
RP SEQUENCE OF 35-107 FROM N.A.
RA Jang J.S., Kim B.E.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP STRUCTURE BY NMR OF 39-107.
RX MEDLINE=20069929; PubMed=10600366;
RA Qian Y.Q., Johanson K.O., McDevitt P.;
RT "Nuclear magnetic resonance solution structure of truncated human
RT GRObeta [5-73] and its structural comparison with CXCL chemokine
RT family members GROalpha and IL-8.";
RL J. Mol. Biol. 294:1085-1072(1999).
CC -!- FUNCTION: PRODUCED BY ACTIVATED
CC EXPRESSED AT SITES OF INFLAMMATION.
CC -!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXCL).

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 CC -----

DR EMBL; X53799; CAA37808.1; -;
 DR EMBL; M36820; AAA63183.1; -;
 DR EMBL; M57731; AAA63182.1; -;
 DR EMBL; AF043340; AAC03540.1; -;
 DR PIR; JH0281; JH0281;
 DR PDB; 1QNK; 04-FEB-00.
 DR MIM; 139110; -;
 DR InterPro; IPR001089; -;
 DR InterPro; IPR001811; -;
 DR InterPro; IPR002473; -;
 DR Pfam; PF00048; IL8; 1;
 DR PRINTS; PR00436; INTERLEUKIN8.
 DR PRINTS; PR00437; SMALLCYTOKINE_CXC.
 DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
 CC Cytokine; Chemotaxis; Inflammatory response; Signal; 3D-structure.
 CC SIGNAL 1 34
 CC CHAIN 35 107 MACROPHAGE INFLAMMATORY PROTEIN-
 CC 2-ALPHA.
 FT DISULFID 43 69
 FT DISULFID 45 85
 SQ SEQUENCE 107 AA; 11389 MW; 740F277E928571BA CRC64;

Query Match 100.0%; Score 379; DB 1; Length 107;
 Best Local Similarity 100.0%; Pred. No. 2.4e-36;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APLATELCOCLOGIHLKNIQSVKSPGPHCAQTEVIATLKNGKACLNPAWPK 60
 DB 35 APLATELCOCLOGIHLKNIQSVKSPGPHCAQTEVIATLKNGKACLNPAWPK 94
 QY 61 KIIEKMLKNGKSN 73
 DB 95 KIIEKMLKNGKSN 107

RESULT 2
 GRO_HUMAN STANDARD; PRT; 107 AA.
 AC P09341;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 CC GROWTH REGULATED PROTEIN PRECURSOR (MELANOMA GROWTH STIMULATORY
 CC ACTIVITY) (MGSA) (NEUTROPHIL-ACTIVATING PROTEIN 3) (NAP-3).
 GN SCYB1 OR GRO1 OR GROA OR GRO OR MGSA.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88041072; PubMed=2890161;
 RA Anisowicz A., Bardwell L., Sager R.;
 RT "Constitutive overexpression of a growth-regulated gene in
 RT transformed Chinese hamster and human cells";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:7188-7192(1987).
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=88328991; PubMed=2970963;
 RA Richmond A., Balentien E., Thomas H.G., Flagg G., Barton D.E.,
 RA Spiess J., Bordon R., Francke U., Derynck R.;
 RT "Molecular characterization and chromosomal mapping of melanoma
 RT growth stimulatory activity, a growth factor structurally related to
 RT beta-thromboglobulin";
 RL EMBO J. 7:2025-2033(1988).

RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=91057157; PubMed=2129556;
 RA Baker N.E., Kucera G., Richmond A.;
 RT "Nucleotide sequence of the human melanoma growth stimulatory
 RT activity (MGSA) gene";
 RL Nucleic Acids Res. 18:6453-6453(1990).
 RN [4]
 RP SEQUENCE OF 35-65.
 RX MEDLINE=90217938; PubMed=2182761;
 RA Schroeder J.-M., Persoon N.L.M., Christophers E.;
 RT "Lipopolysaccharide-stimulated human monocytes secrete, apart from
 RT neutrophil-activating peptide 1/interleukin 8, a second neutrophil-
 RT activating protein. NH2-terminal amino acid sequence identity with
 RT melanoma growth stimulatory activity";
 RL J. Exp. Med. 171:1091-1100(1990).
 RN [5]
 RP SEQUENCE OF 35-57.
 RX MEDLINE=89246368; PubMed=2655583;
 RA Golds E.E., Mason P., Nyirkos P.;
 RT "Inflammatory cytokines induce synthesis and secretion of gro protein
 RT and a neutrophil chemotactic factor but not beta 2-microglobulin in
 RT human synovial cells and fibroblasts";
 RL Biochem. J. 259:585-588(1989).
 RN [6]
 RP POSSIBLE FUNCTION.
 RX MEDLINE=89356650; PubMed=2670560;
 RA Wen D., Rowland A., Derynck R.;
 RT "Expression and secretion of gro/MGSA by stimulated human endothelial
 RT cells";
 RL EMBO J. 8:1761-1766(1989).
 RN [7]
 RP STRUCTURE BY NMR.
 RX MEDLINE=93387459; PubMed=8397104;
 RA Fairbrother W.J., Reilly D., Colby T., Horuk R.;
 RT "1H assignment and secondary structure determination of human
 RT melanoma growth stimulating activity (MGSA) by NMR spectroscopy";
 RL FEBS Lett. 330:302-306(1993).
 RN [8]
 RP STRUCTURE BY NMR.
 RX MEDLINE=94376296; PubMed=8089846;
 RA Fairbrother W.J., Reilly D., Colby T., Hesselgesser J., Horuk R.;
 RT "The solution structure of melanoma growth stimulating activity";
 RL J. Mol. Biol. 242:252-270(1994).
 RN [9]
 RP STRUCTURE BY NMR.
 RX MEDLINE=95105175; PubMed=7806518;
 RA Kim K.S., Clark-Lewis I., Sykes B.D.;
 RT "Solution structure of GRO/melanoma growth stimulatory activity
 RT determined by 1H NMR spectroscopy";
 RL J. Biol. Chem. 269:32909-32915(1994).
 CC -1- FUNCTION: HAS CHEMOTACTIC ACTIVITY FOR NEUTROPHILS. MAY PLAY A
 CC ROLE IN INFLAMMATION AND EXERTS ITS EFFECTS ON ENDOTHELIAL CELLS
 CC IN AN AUTOCRINE FASHION.
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
 CC C-X-C) (CHEMOKINE CXC).
 CC -----
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 CC -----
 CC EMBL; J03561; AAA35933.1; -;
 DR EMBL; X12510; CAA31027.1; -;
 DR EMBL; X54489; CAA38361.1; -;
 DR PIR; A28414; A28414.
 DR PIR; S00983; S00983.
 DR PIR; S03976; S03976.
 DR PIR; S13669; S13669.

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or send an email to licensee@isb-sib.ch).

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EMBL; X53800; CAA37809.1; --
EMBL; M36821; AAA63184.1; --
PIR; B38290; B38290.
PIR; JH0282; JH0282.
HSSP; P09341; IMGs.
MIM; I39111; --
InterPro; IPR001089; --
InterPro; IPR001811; --
InterPro; IPR002473; --
Pfam; PF00048; IL8; 1.
PRINTS; PR00436; INTERLEUKIN8.
DR PRINTS; PR00437; SMALLCYTRCXC.
PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
CytoKine; Chemotaxis; Inflammatory response; Signal.

KW SIGNAL
FT CHAIN 1 34 MACROPHAGE INFLAMMATORY PROTEIN-
FT CHAIN 35 107 2-BETA.
FT FT BY SIMILARITY.
FT DISULFID 43 69 BY SIMILARITY.
FT DISULFID 45 85 BY SIMILARITY.
FT CONFLICT 27 28 AA -> G (IN REF. 2).
SQ SEQUENCE 107 AA; II342 MW; 97A69946B7F1F070 CRC64;

Query Match 85.8%; Score 325; DB 1; Length 107;
Best Local Similarity 83.6%; Pred No. 3,2e-30;
Matches 61; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 APLATELRCCQLQTLOGIHLNKISVKVSGPGHPCAQTEVIATLKGAKCLNPASPMVK 60
 | : ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
DB 35 ASVTVELRCQCLOLTGIIHLANIQSNNVRSPGPCHCAQTEVIATLKGKKACLNPA
QY 61 KIEIKMLKNKGSN 73
 ||||| : | : |
DB 95 KIEIKMLKNKGSN 107

RESULT 4

GRO_CRIGR ID GRO_CRIGR STANDARD; PRT; 101 AA.

P09340; AC

DT DT 01-MAR-1989 (Rel. 10, Created)

DT DT 01-MAR-1989 (Rel. 10, Last sequence update)

DT DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE DE GROWTH REGULATED PROTEIN PRECURSOR.

GN SCYBI OR GRO.

OS Cricetusulus griseus (Chinese hamster).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Cricetinae;
OC Cricetulus.

OX NCBI_Taxid=10029;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=88041072; PubMed=2890161;
RA Anisowicz A., Bardwell L.; Seger R.;
RT "Constitutive overexpression of a growth-regulated gene in transformed Chinese hamster and human cells";
RL Proc. Natl. Acad. Sci. U.S.A. 84:7188-7192(1987).
CC -! FUNCTION: HAS CHEMOTACTIC ACTIVITY FOR NEUTROPHILS.
CC -! SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE C-X-C) (CHEMOKINE CXC).

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EMBL; J03560; AAA36985.1; --

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DR PIR; B28414; B28414.
DR HSP; P10889; IMI2.
DR InterPro; IPR001089; -.
DR InterPro; IPR001811; -.
DR InterPro; IPR002473; -.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR PRINTS; PR00437; SMALL_CYTOKINES_CXC; 1.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW Cytokine; Growth factor; Inflammatory response; Signal.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 101 GROWTH REGULATED PROTEIN.
FT DISULFID 37 63 BY SIMILARITY.
FT DISULFID 39 79 BY SIMILARITY.
FT SEQUENCE 101 AA; 10893 MW; 666PB7E9CC512019 CRC64;

Query Match 80.2%; Score 304; DB 1; Length 101;
Best Local Similarity 77.1%; Pred. No. 7.4e-28;
Matches 54; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

Oy 1 APLATELCOCLOTLOGIHLKNIQSVKSPGPHCAQTEVIATLKGKACLNPAAPMVK 60
    ||:|||||||:|:|||||||:|:|||||||:|||||||:|||||||:|:|:
Db 29 APVANELRCOCLOTMTGVLKNIQSLKVTTPPGPHCTQTEVIATLKGQEAACLNPAAPMVQ 88
    ||:|||||||:|:|||||||:|:|||||||:|||||||:|||||||:|:|:
Oy 61 KIIEKMLKNG 70
    ||:|||||||:
Db 89 KIVQKMLKSG 98
    ||:|||||||:

RESULT 5
GRO_SHEEP
ID GRO_SHEEP STANDARD; PRT; 103 AA.
AC O46678;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE GROWTH REGULATED PROTEIN PRECURSOR.
GN SCYB1 OR GRO.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Yoshimura T., Modi W.S.;
RT "Isolation of novel GRO genes, and a phylogenetic analysis of the CXC
chemokine subfamily in mammals."
Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: HAS CHEMOTACTIC ACTIVITY FOR NEUTROPHILS.
-!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
C-X-C) (CHEMOKINE CXC).
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-----
EMBL; U95814; AAB93930.1; -.
HSP; P09341; IMGs.
InterPro; IPR001089; -.
InterPro; IPR001811; -.
InterPro; IPR002473; -.
Pfam; PF00048; IL8; 1.
PRINTS; PR00436; INTERLEUKIN8.
PRINTS; PR00437; SMALL_CYTOKINES_CXC; 1.
PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW Cytokine; Growth factor; Inflammatory response; Signal.
FT SIGNAL 1 30 POTENTIAL.

```

```

FT CHAIN 31 103 GROWTH REGULATED PROTEIN.
FT DISULFID 39 65 BY SIMILARITY.
FT DISULFID 41 81 BY SIMILARITY.
SQ SEQUENCE 103 AA; 10820 MW; C59857F346716695 CRC64;

Query Match 80.2%; Score 304; DB 1; Length 103;
Best Local Similarity 76.7%; Pred. No. 7.5e-28;
Matches 56; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

Oy 1 APLATELCOCLOTLOGIHLKNIQSVKSPGPHCAQTEVIATLKGKACLNPAAPMVK 60
    ||:|||||||:|:|||||||:|:|||||||:|||||||:|||||||:|:|:
Db 31 APVANELRCOCLOTQVGIHLKNIQSVKVTTPPGPHGQTEVIATLKGQEVCLNPAAPMVK 90
    ||:|||||||:|:|||||||:|:|||||||:|||||||:|||||||:|:|:
Oy 61 KIIEKMLKNGKSN 73
    ||:|||||||:
Db 91 KIIDKMLNQASN 103
    ||:|||||||:

RESULT 6
GRO_BOVIN
ID GRO_BOVIN STANDARD; PRT; 98 AA.
AC O46675;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GROWTH REGULATED PROTEIN HOMOLOG GAMMA PRECURSOR (GRO-GAMMA).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Yoshimura T., Modi W.S.;
RT Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
-!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
C-X-C) (CHEMOKINE CXC).
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-----
EMBL; U95811; AAB93927.1; -.
InterPro; IPR001089; -.
InterPro; IPR001811; -.
Pfam; PF00048; IL8; 1.
PRINTS; PR00437; SMALL_CYTOKINES_CXC; 1.
PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW Cytokine; Growth factor; Inflammatory response; Signal.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 98 GROWTH REGULATED PROTEIN HOMOLOG GAMMA.
FT DISULFID 39 65 BY SIMILARITY.
FT DISULFID 41 81 BY SIMILARITY.
SQ SEQUENCE 98 AA; 10393 MW; 942CD6897C21EDE9 CRC64;

Query Match 79.2%; Score 300; DB 1; Length 98;
Best Local Similarity 83.6%; Pred. No. 2e-27;
Matches 56; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Oy 1 APLATELCOCLOTLOGIHLKNIQSVKSPGPHCAQTEVIATLKGKACLNPAAPMVK 60
    ||:|||||||:|:|||||||:|:|||||||:|||||||:|||||||:|:|:
Db 31 APVANELRCOCLOTQVGIHLKNIQSVKVTTPPGPHDQTEVIATLKGQEVCLNPAAPMVK 90
    ||:|||||||:|:|||||||:|:|||||||:|||||||:|||||||:|:|:
Oy 61 KIIEKML 67
    ||:|||||||:
Db 91 KIIDKML 97
    ||:|||||||:

```

```
RESULT 7
GROA_BOVIN
ID GROA_BOVIN STANDARD; PRT; 104 AA.
AC O46676;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GROWTH REGULATED PROTEIN HOMOLOG ALPHA PRECURSOR (GRO-ALPHA).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RA SEQUENCE FROM N.A.
Yoshimura T., Modi W.S.;
Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
-!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
C-X-C) (CHEMOKINE CXCL)
-----
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-----
DR EMBL; U95812; AAB93928.1; -.
DR InterPro; IPR001089; -.
DR InterPro; IPR001811; -.
DR InterPro; IPR002473; -.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR PROSITE; PS00437; SMALL_CYTOKINES_CXC.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW Cytokine; Growth factor; Inflammatory response; Signal.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 104 GROWTH REGULATED PROTEIN HOMOLOG ALPHA.
FT DISULFID 40 66 BY SIMILARITY.
FT DISULFID 42 82 BY SIMILARITY.
SQ SEQUENCE 104 AA; 10984 MW; 1002CAC064DB1F76 CRC64;
-----
Query Match 78.9%; Score 299; DB 1; Length 104;
Best Local Similarity 75.3%; Pred. No. 2.8e-27;
Matches 55; Conservative 7; Mismatches 11; Indels 0; Gaps 0;
QY 1 APLATELRCCQLTQLOGIHLKNIQSVKSPGPHCAQTEVITLKNQKACLNAPSPVMK 60
DQ 32 APVYNELRCQCLTQLOGIHLKNIQSVKVTTPGPHCDQTEVIASLTQGEVCLNPTAPVMK 91
QY 61 KIIEKMLKNGKSN 73
DQ 92 KIIDKMLNKASAN 104
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RESULT 8
GROB_BOVIN
ID GROB_BOVIN STANDARD; PRT; 104 AA.
AC O46677;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GROWTH REGULATED PROTEIN HOMOLOG BETA PRECURSOR (GRO-BETA).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RA SEQUENCE FROM N.A.
```

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RA Yoshimura T., Modi W.S.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXCL)
-----
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-----
DR EMBL; U95813; AAB93929.1; -.
DR InterPro; IPR001089; -.
DR InterPro; IPR001811; -.
DR InterPro; IPR002473; -.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR PROSITE; PS00437; SMALL_CYTOKINES_CXC.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW Cytokine; Growth factor; Inflammatory response; Signal.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 104 GROWTH REGULATED PROTEIN HOMOLOG BETA.
FT DISULFID 40 66 BY SIMILARITY.
FT DISULFID 42 82 BY SIMILARITY.
SQ SEQUENCE 104 AA; 10950 MW; 40A8C06A64D67F7B CRC64;
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Query Match 78.9%; Score 299; DB 1; Length 104;
Best Local Similarity 75.3%; Pred. No. 2.8e-27;
Matches 55; Conservative 7; Mismatches 11; Indels 0; Gaps 0;
QY 1 APLATELRCCQLTQLOGIHLKNIQSVKSPGPHCAQTEVITLKNQKACLNAPSPVMK 60
DQ 32 APVYNELRCQCLTQLOGIHLKNIQSVKVTTPGPHCDQTEVIASLTQGEVCLNPTAPVMK 91
QY 61 KIIEKMLKNGKSN 73
DQ 92 KIIDKMLNKASAN 104
-----
RESULT 9
GRO1_RABIT
ID GRO1_RABIT STANDARD; PRT; 71 AA.
AC P30782;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PERMEABILITY FACTOR 2 (RPF2) (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RA SEQUENCE FROM N.A.
RC STRAIN-NEW ZEALAND WHITE; TISSUE=Alveolar macrophage;
RX MEDLINE=95129889; PubMed=7828903;
RA Johnson M.C., Goodman R.B. II, Kajikawa O., Wong V.A., Mongovin S.M.,
RA Martin T.R.;
RT "Cloning of two rabbit GRO homologues and their expression in
RT alveolar macrophages.";
RL Gene 151:337-338(1994).
RN [2]
RP SEQUENCE OF 1-36.
RC STRAIN-NEW ZEALAND WHITE; TISSUE=Peritoneal cavity;
RX MEDLINE=91378900; PubMed=1898341;
RA Jose P.J., Collins P.D., Perkins J.A., Beaubien B.C., Totty N.F.,
RA Waterfield M.D., Hsuan J., Williams T.J.;
RT "Identification of a second neutrophil-chemoattractant cytokine
RT generated during an inflammatory reaction in the rabbit peritoneal
RT cavity in vivo. Purification, partial amino acid sequence and
RT structural relationship to melanoma-growth-stimulatory activity.";
```

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CC	-----	
DR	EMBL; U12310; AAA20487.1; -	
DR	HSP; P09341; 1MGs.	
DR	InterPro: IPR001089; -	
DR	InterPro: IPR001811; -	
DR	InterPro: IPR002473; -	
DR	Pfam; PF00048; IL8; 1.	
DR	PRINTS; PR00436; INTERLEUKIN8.	
DR	PRINTS; PR00437; SMALLCYTKCX.	
DR	PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.	
KW	Cytokine; Growth factor; Inflammatory response; Signal.	
FT	SIGNAL 1 31 PROBABLE.	
FT	CHAIN 32 104 GROWTH REGULATED PROTEIN HOMOLOG.	
FT	DISULFID 40 66 BY SIMILARITY.	
FT	DISULFID 42 82 BY SIMILARITY.	
SQ	SEQUENCE 104 AA; 10900 MW; 10B9D07B65C77F67 CRC64;	
	Query Match 77.8%; Score 295; DB 1; Length 104;	
	Best Local Similarity 74.0%; Pred. No. 7.9e-27;	
	Matches 54; Conservative 8; Mismatches 11; Indels 0; Gaps	
QY	1 APLATELRCQCLQTQGIHLKNIQSVKSPGPHCAQTEVIATLKNQKACLNPASPVMK 60	
DB	:	
DB	32 APYVNELRCQCLQTQGIHLKNIQSVKVTTPGPHCDQTEVIASLTKGQEVCLNPATPVK 91	
QY	61 KIIEKMLKNKSN 73	
DB	:	
DB	92 KIIDKMLNKASAN 104	
RESULT	11	
GRO_RAT		
ID	GRO_RAT STANDARD; PRT; 96 AA.	
AC	P14095;	
DT	01-JAN-1990 (Rel. 13, Created)	
DT	01-NOV-1995 (Rel. 32, Last sequence update)	
DT	01-OCT-2000 (Rel. 40, Last annotation update)	
DE	GROWTH REGULATED PROTEIN PRECURSOR (CYTOKINE-INDUCED NEUTROPHIL	
DE	CHEMOATTRACTANT) (CINC-1) (PLATELET-DERIVED GROWTH FACTOR-INDUCIBLE	
DE	PROTEIN KC).	
GN	SCYB1 OR GRO.	
OS	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
OX	NCBI_Taxid=10116;	
RP	[1]	
RP	SEQUENCE FROM N.A.	
RP	MEDLINE=93246259; PubMed=8482545;	
RX	Konishi K, Tanaka Y, Yamamoto M, Yomogida K., Watanabe K.,	
RA	Tsurufuji S., Fujioka M.;	
RA	"Structure of the gene encoding rat neutrophil chemo-attractant Gro."	
RT	Gene 126:285-286(1993).	
RP	[2]	
RP	SEQUENCE FROM N.A.	
RP	MEDLINE=92246987; PubMed=1374243;	
RX	Huang S., Paulauskis J., Kobzik L.;	
RA	"Rat KC cDNA cloning and mRNA expression in lung macrophages and	
RT	fibroblasts.";	
RT	Biochem. Biophys. Res. Commun. 184:922-929(1992).	
RP	[3]	
RP	SEQUENCE OF 25-96.	
RX	MEDLINE=90062049; PubMed=2684956;	
RA	Watanabe K., Konishi K., Fujioka M., Kinoshita S., Nakagawa H.;	
RA	"The neutrophil chemoattractant produced by the rat kidney	
RT	epitheloid cell line NRK-52E is a protein related to the KC/gro	
RT	protein.";	
RL	J. Biol. Chem. 264:19559-19563(1989).	
RP	[4]	
RP	SEQUENCE OF 36-88 FROM N.A.	
RP	TISSUE=Lung;	
RX	MEDLINE=93035653; PubMed=1415488;	

RA Huang S., Paulauskis J.D., Godleski J.J., Kobzik L.;
 RT "Expression of macrophage inflammatory protein-2 and KC mRNA in
 RT pulmonary inflammation.";
 RL Am. J. Pathol. 141:981-988(1992).
 RN [5]
 RP SEQUENCE OF 25-56.
 RC STRAIN=WISTAR;
 RX MEDLINE=96183056; PubMed=8607872;
 RA Nakagawa H., Shiota S., Takano K., Shibata F., Kato H.;
 RT "Cytokine-induced neutrophil chemoattractant (CINC)-2 alpha, a novel
 RT member of rat GRO/CINCS, is a predominant chemokine produced by
 RT lipopolysaccharide-stimulated rat macrophages in culture.";
 RL Biochem. Biophys. Res. Commun. 220:945-948(1996).
 RN [6]
 RP STRUCTURE BY NMR.
 RX MEDLINE=95046335; PubMed=7957925;
 RA Hanzawa H., Hanyama H., Watanabe K., Tsurufuji S.;
 RT "The three dimensional structure of rat cytokine CINC/gro in solution
 RT by homonuclear 3D NMR.";
 RL FEBS Lett. 354:207-212(1994).
 RN [7]
 RP STRUCTURE BY NMR.
 RX MEDLINE=97335927; PubMed=9192722;
 RA Hanzawa H., Hanyama H., Konishi K., Watanabe K., Tsurufuji S.;
 RT "Subunit association and monomer structure of CINC/Gro revealed by
 RT 1H-NMR.";
 RL J. Biochem. 121:835-841(1997).
 RN [8]
 RP STRUCTURE BY NMR.
 RX MEDLINE=98162936; PubMed=9504410;
 RA Hanzawa H., Hanyama H., Konishi K., Watanabe K., Tsurufuji S.;
 RT "Solution structure of CINC/Gro investigated by heteronuclear NMR.";
 RL J. Biochem. 123:62-70(1998).
 CC -!- FUNCTION: HAS CHEMOTACTIC ACTIVITY FOR NEUTROPHILS. CONTRIBUTES TO
 CC NEUTROPHIL ACTIVATION DURING INFLAMMATION.
 CC -!- SUBUNIT: MONOMER AND HOMODIMER.
 CC -!- TISSUE SPECIFICITY: AT LEAST EXPRESSED IN THE LUNG AND TRACHEA.
 CC -!- INDUCTION: IN LUNG, BY LIPOPOLYSACCHARIDE OR INFLAMMATION.
 CC -!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
 CC C-X-C) (CHEMOKINE CXCL).
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 DR EMBL; D11445; BAA02009.1; -;
 DR EMBL; D11444; BAA02008.1; -;
 DR EMBL; M86536; AAA42053.1; -;
 DR EMBL; S45856; -; NOT_ANNOTATED_CDS.
 DR PIR; A34481; A34481.
 DR HSP; P09341; IMSH.
 DR InterPro; IPR001089; -;
 DR InterPro; IPR001811; -;
 DR InterPro; IPR002473; -;
 DR Pfam; PF00048; IL8; 1.
 DR PRINTS; PR00436; INTERLEUKIN8.
 DR PRINTS; PR00437; SMALLCYTOKC.
 DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
 KW Cytokine; Growth factor; Inflammatory response; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 96 GROWTH REGULATED PROTEIN.
 FT DISULFID 33 59 BY SIMILARITY.
 FT DISULFID 35 75 BY SIMILARITY.
 FT SEQUENCE 96 AA; 10249 MW; 6046C9E2C2582652 CRC64;
 SQ

Query Match 74.9%; Score 284; DB 1; Length 96;
 Best Local Similarity 75.08; Pred. No. 1.3e-25;
 Matches 51; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 APLATELRCCLOTLQIHLKNTQSVKVPKPGPHCAQTEVIATLKNQKACLNAPSPMWK 60
 DB 25 APVANELRCLOTLQVAGIHFKNIQSLKVPMPGPHCTQTEVIATLKNQKACLNAPSPMWK 84
 QY 61 KIIEKMLK 68
 DB 85 KIYQKMLK 92
 RESULT 12
 GRO_MOUSE STANDARD; PRT; 96 AA.
 AC P12850;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE GROWTH REGULATED PROTEIN PRECURSOR (PLATELET-DERIVED GROWTH FACTOR-
 DE INDUCIBLE PROTEIN KC) (SECRETORY PROTEIN N51).
 GN SCYB1 OR GRO1 OR GRO OR MGSA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89139485; PubMed=2917992;
 RA Oquendo P., Alberta J., Wen D., Graycar J.L., Derynck R., Stiles C.D.;
 RT "The platelet-derived growth factor-inducible KC gene encodes a
 RT secretory protein related to platelet alpha-granule proteins.";
 RL J. Biol. Chem. 264:4133-4137(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89078502; PubMed=2909392;
 RA Ryseck R.P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;
 RT "Cloning and sequence of a secretory protein induced by growth
 RT factors in mouse fibroblasts.";
 RL Exp. Cell Res. 180:266-275(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96016008; PubMed=7561058;
 RA Ohmori Y., Fukumoto S., Hamilton T.A.;
 RT "Two structurally distinct kappa B sequence motifs cooperatively
 RT control LPS-induced KC gene transcription in mouse macrophages.";
 RL J. Immunol. 155:3593-3600(1995).
 CC -!- FUNCTION: HAS CHEMOTACTIC ACTIVITY FOR NEUTROPHILS. CONTRIBUTES TO
 CC NEUTROPHIL ACTIVATION DURING INFLAMMATION (BY SIMILARITY).
 CC -!- INDUCTION: BY PLATELET-DERIVED GROWTH FACTOR. IN LUNG, BY
 CC LIPOPOLYSACCHARIDE OR INFLAMMATION (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
 CC C-X-C) (CHEMOKINE CXCL).
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 CC -----
 DR EMBL; J04596; AAA40131.1; -;
 DR EMBL; U20634; AAB03376.1; -;
 DR EMBL; U20527; AAB03376.1; JOINED.
 DR EMBL; S79767; -; NOT_ANNOTATED_CDS.
 DR PIR; A32954; A32954.
 DR PIR; JH0081; JH0081.

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DR HSP: P09341; lmsH.
DR MGD; MGI:108068; Grol.
DR InterPro; IPR001089; -.
DR InterPro; IPR001811; -.
DR InterPro; IPR002473; -.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR PRINTS; PR00437; SMALLCYTOKINE.
DR PROSITE; PS00471; SMALLCYTOKINES_CXC; 1.
KW Cytokine; Growth factor; Inflammatory response; Signal.
FT SIGNAL 1 24 PROBABLE.
FT CHAIN 25 96 GROWTH REGULATED PROTEIN.
FT DISULFID 33 59 BY SIMILARITY.
FT DISULFID 35 75 BY SIMILARITY.
SQ SEQUENCE 96 AA; 10254 MW; 4A52B5E5C38B45C2 CRC64;

Query Match 73.4%; Score 278; DB 1; Length 96;
Best Local Similarity 73.5%; Pred. No. 6.2e-25;
Matches 50; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

1 APLATELRCCQCLQTLOGIHLKNIQSVKSPGPHCAQTEVIATLKGOKACLNPA5PMVK 60
II:IIIIIIII:IIIIIIII:IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII:II:II:
25 APLATELRCCQCLQTLOGIHLKNIQSVKSPGPHCAQTEVIATLKGOKACLNPA5PMVK 84
II:IIIIIIII:IIIIIIII:IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII:II:II:
QY 61 KIIEKMLK 68
II:IIIIII
DB 85 KIVQKMLK 92

RESULT 13
MIP2_MOUSE
ID MIP2_MOUSE STANDARD; PRT; 100 AA.
AC P10889;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE MACROPHAGE INFLAMMATORY PROTEIN 2 PRECURSOR (MIP2).
GN SCYB2 OR MIP2 OR MIP-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90354792; PubMed=2201751;
RA Tekamp-Olson P., Gallegos C., Bauer D., McClain J., Sherry B.,
RA Fabre M., van Deventer S., Cerami A.;
RT "Cloning and characterization of cDNAs for murine macrophage
inflammatory protein 2 and its human homologues.";
J. Exp. Med. 172:911-919(1990).
RN [2]
RP SEQUENCE OF 28-59.
RX MEDLINE=89098980; PubMed=2643119;
RA Wolpe S.D., Sherry B., Juers D., Davatellis G., Yurt R.W., Cerami A.;
RT "Identification and characterization of macrophage inflammatory
protein 2.";
Proc. Natl. Acad. Sci. U.S.A. 86:612-616(1989).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE=98285558; PubMed=9622482;
RA Shao W., Jerva L.F., West J., Lolis E., Schweitzer B.I.;
RT "Solution structure of murine macrophage inflammatory protein-2.";
Biochemistry 37:8303-8313(1998).
CC -!- FUNCTION: CHEMOTACTIC FOR HUMAN POLYMONOPHONUCLEAR LEUKOCYTES BUT
DOES NOT INDUCE CHEMOKINESIS OR AN OXIDATIVE BURST.
CC -!- SUBUNIT: HOMOTETRAMER.
CC -!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
C-X-C) (CHEMOKINE CXC).
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CC EMBL; X53798; CAA37807.1; -.
DR PIR; JH0200; JH0200.
DR PDB; 1MI2; 29-APR-98.
DR MGD; MGI:1340094; Scyb2.
DR InterPro; IPR001089; -.
DR InterPro; IPR001811; -.
DR InterPro; IPR002473; -.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR PRINTS; PR00437; SMALLCYTOKINE.
DR PROSITE; PS00471; SMALLCYTOKINES_CXC; 1.
KW Cytokine; Chemotaxis; Inflammatory response; Signal; 3D-structure.
FT SIGNAL 1 27
FT CHAIN 28 100 MACROPHAGE INFLAMMATORY PROTEIN 2.
FT DISULFID 36 62
FT DISULFID 38 78
SQ SEQUENCE 100 AA; 10621 MW; B9EF0A3218EE92B5 CRC64;

Query Match 68.9%; Score 261; DB 1; Length 100;
Best Local Similarity 65.8%; Pred. No. 5.5e-23;
Matches 48; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 1 APLATELRCCQCLQTLOGIHLKNIQSVKSPGPHCAQTEVIATLKGOKACLNPA5PMVK 60
II:IIIIIIII:II:IIII:IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII:II:II:
28 AVASELRCCQCLKTPRVDFKNIQSLVTPPGPHCAQTEVIATLKGOKVCLDPEAPLVQ 87
II:IIIIIIII:II:IIII:IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII:II:II:
QY 61 KIIEKMLKGNKSN 73
II:II:II:II:II:
DB 88 KIIQILNKGRAN 100

RESULT 14
GRO_CAVPO
ID GRO_CAVPO STANDARD; PRT; 104 AA.
AC O5235;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE GROWTH REGULATED PROTEIN PRECURSOR.
GN SCYB1 OR GRO.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=STRAIN 2;
RA Yoshimura T., Modi W.S.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HARTLEY WHITE; TISSUE=Spleen;
RA Yoshimura T., Takeya M., Ogata H., Gillitzer R.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: HAS CHEMOTACTIC ACTIVITY FOR NEUTROPHILS.
CC -!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
C-X-C) (CHEMOKINE CXC).
-----
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CC EMBL; U95809; AAB93925.1; -.
DR
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```

RX MEDLINE=94318061; PubMed=8043001;
RA Nakagawa H., Komorita N., Shibata F., Ikesue A., Konishi K.,
RA Fujioaka M., Kato H.;
RT "Identification of cytokine-induced neutrophil chemoattractants
RT (CINC), rat GRO/CINC-2 alpha and CINC-2 beta, produced by granulation
RT tissue in culture: purification, complete amino acid sequences and
RT characterization.;"
RL Biochem. J. 301:545-550(1994).
RN [6]
RP SEQUENCE OF 32-59.
RC STRAIN-WISTAR;
RA MEDLINE=96183056; PubMed=8607872;
RA Nakagawa H., Shiota S., Takano K., Shibata F., Kato H.;
RT "Cytokine-induced neutrophil chemoattractant (CINC)-2 alpha, a novel
RT member of rat GRO/CINCS, is a predominant chemokine produced by
RT lipopolysaccharide-stimulated rat macrophages in culture.;"
RL Biochem. Biophys. Res. Commun. 220:945-948(1996).
CC -1- FUNCTION: CHEMOTACTIC FOR HUMAN POLYMORPHONUCLEAR LEUKOCYTES BUT
CC DOES NOT INDUCE CHEMOKINESIS OR AN OXIDATIVE BURST. CONTRIBUTES TO
CC NEUTROPHIL ACTIVATION DURING INFLAMMATION.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- TISSUE SPECIFICITY: AT LEAST EXPRESSED IN THE LUNG AND TRACHEA.
CC -1- INDUCTION: IN LUNG, BY LIPOPOLYSACCHARIDE OR INFLAMMATION.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXCL).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X65647; CAA65599.1; -.
DR EMBL; S77604; AAB33749.1; -.
DR EMBL; U45965; AAA92438.1; -.
DR EMBL; S45855; -. NOT_ANNOTATED_CDS.
DR PTR; S21467; S21467.
DR HSP; P10889; IWI2.
DR InterPro; IPR001089; -.
DR InterPro; IPR001811; -.
DR InterPro; IPR002473; -.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR PRINTS; PR00437; SMALLCYTOKXC.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
DR Cytokine; Chemotaxis; Inflammatory response; Signal.
KW SIGNAL
FT SIGNAL 1 31
FT CHAIN 32 100 MACROPHAGE INFLAMMATORY PROTEIN 2.
FT DISULFID 36 62 BY SIMILARITY.
FT DISULFID 38 78 BY SIMILARITY.
FT SEQUENCE 100 AA; 10783 MW; 4299DFE86FF37A9B CRC64;
SQ
Query Match 65.7%; Score 249; DB 1; Length 100;
Best Local Similarity 62.0%; Pred. No. 1.3e-21;
Matches 44; Conservative 14; Mismatches 13; Indels 0; Gaps 0;
QY 3 LATELRQCQLQTLOGIHLKNTQSVKVSPPGPHCAQTEVIATFLKNGQKACLNPA SPVYKI 62
Db 30 VASELRQCQLTTPRVDFKNITQSLVTTPPGPHCAQTEVIATFLKDGHEVCLNPEAPLVQRI 89
QY 63 IEKMLKNGKSN 73
Db 90 VQILNKNGKAN 100

```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 4, 2001, 07:35:28 ; Search time 19.46 Seconds
(without alignments)
439.680 Million cell updates/sec

Title: US-09-467-160-3

Perfect score: 379

Sequence: 1 APLATELRQCQLTQGIHL.....PASPVMVKIIEKMLKNGKSN 73

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Aligned: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL15:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_unclassified:*
- 13: sp_vertebrate:*
- 14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	300	79.2	108	6 Q28724	Q28724 oryctolagus
2	241	63.6	59	6 Q2764	Q2764 equus caball
3	179.5	47.4	104	13 Q73912	Q73912 gallus gall
4	170.5	45.0	105	11 Q92126	Q92126 mus musculus
5	141.5	37.3	101	6 Q9XSX5	Q9XSX5 felis silve
6	137	36.1	33	11 Q9QU07	Q9QU07 rattus sp.
7	133	35.1	54	4 Q9UC64	Q9UC64 homo sapien
8	129	34.0	48	6 Q9TR91	Q9TR91 bos taurus
9	125.5	33.1	134	14 Q9YVAG	Q9YVAG gallid herp
10	125.5	33.1	142	14 Q9IBJ7	Q9IBJ7 turkey herp
11	125.5	33.1	203	14 Q67634	Q67634 gallid herp
12	123	32.5	31	6 Q97800	Q97800 bos taurus
13	117	30.9	101	13 Q93442	Q93442 lampetra fl
14	108	28.5	34	11 Q9QV88	Q9QV88 rattus sp.
15	107	28.2	40	11 Q9QV74	Q9QV74 rattus sp.
16	105.5	27.8	41	6 Q9XSD2	Q9XSD2 oryctolagus
17	90.5	23.9	86	11 Q9QX28	Q9QX28 mus musculus
18	88.5	23.4	99	11 Q9JHH7	Q9JHH7 mus musculus
19	87.5	23.1	111	4 Q9NS21	Q9NS21 homo sapien

20	78	20.6	100	11 Q9JHH5	Q9JHH5 mus musculus
21	77.5	20.4	89	11 Q9QZD1	Q9QZD1 rattus norv
22	74.5	19.7	159	14 Q68406	Q68406 human cytom
23	74	19.5	24	11 Q9QV82	Q9QV82 rattus sp.
24	71.5	18.9	118	14 Q9J2M1	Q9J2M1 macaca mula
25	71.5	18.9	159	14 Q68399	Q68399 human cytom
26	71	18.7	318	5 Q23352	Q23352 caenorhabdi
27	69.5	18.3	93	13 Q9PTF8	Q9PTF8 brachydanio
28	69	18.2	20	11 Q9QUH5	Q9QUH5 rattus sp.
29	69	18.2	710	2 Q32914	Q32914 mycobacteri
30	68.5	18.1	96	13 Q90825	Q90825 gallus gall
31	68	17.9	115	14 Q9WRT7	Q9WRT7 macaca mula
32	65	17.2	2015	5 Q9U5Y1	Q9U5Y1 dictyosteli
33	64.5	17.0	1432	14 Q28851	Q28851 jembrana di
34	63	16.6	20	11 Q9QV73	Q9QV73 rattus sp.
35	62	16.4	510	4 Q9UKZ1	Q9UKZ1 homo sapien
36	62	16.4	688	10 Q9LQW5	Q9LQW5 arabidopsis
37	61.5	16.2	95	14 Q98158	Q98158 kaposi's sa
38	61.5	16.2	471	4 Q60645	Q60645 homo sapien
39	61	16.1	397	10 Q81815	Q81815 arabidopsis
40	61	16.1	617	5 Q96437	Q96437 eimeria ten
41	61	16.1	1212	10 Q9LGT8	Q9LGT8 oryza sativ
42	60.5	16.0	97	6 Q9FTS6	Q9FTS6 bos taurus
43	60.5	16.0	349	1 Q29443	Q29443 archaeoglob
44	60.5	16.0	416	2 Q9X6X2	Q9X6X2 myxococcus
45	60.5	16.0	1880	14 Q92368	Q92368 vesv-like c

ALIGNMENTS

RESULT 1

Q28724 ID Q28724 PRELIMINARY; PRT; 108 AA.

AC Q28724;

DT 01-NOV-1996 (Tremblrel. 01, Created)

DT 01-AUG-1999 (Tremblrel. 11, Last sequence update)

DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)

DE GRO (PERMEABILITY FACTOR 2).

GN RPF2.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NEW ZEALAND WHITE;

RA Yoshimura T., Modi W.S.;

RT "Isolation of novel GRO genes, and a phylogenetic analysis of the CXC

RT chemokine subfamily in mammals."

RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE OF 43-108 FROM N.A.

RC STRAIN=NEW ZEALAND WHITE;

RA MEDLINE=95129889; PubMed=7828903;

RA Johnson M.C., Goodman R.B. II, Kajikawa O., Wong V.A., Mongovin S.M.,

RA Martin T.R.;

RT "Cloning of two rabbit GRO homologues and their expression in alveolar

RT macrophages."

RL Gene 151:337-338(1994).

DR EMBL; U95808; AA933924.1; -;

DR EMBL; L28933; AAA66975.1; -;

DR HSSP; P19875; IQNK.

DR INTERPRO; IPR001089; -;

DR INTERPRO; IPR001811; -;

DR INTERPRO; IPR002473; -;

DR PFAM; PF00048; IL8; 1.

DR PRINTS; PR00436; INTERLEUKIN8.

DR PRINTS; PR00437; SMALLCYTKXC.

DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.

SQ SEQUENCE 108 AA; 11261 MW; 9C278041FC7A5BAD CRC64;

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DE PLATELET FACTOR 4.
GN PF4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL6J; TISSUE=SPLEEN;
RC Watanabe O., Tamari M., Natori K., Kubo S., Shiomoto Y., Nakamura Y.;
RA "Isolation of the murine homologue of rat and human P/platelet factor
RT 4CDNA from the spleen of NOA mouse that is a new atopic dermatitis
RT model by a differential display method.";
RT Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL; AB017491; BAA75660.1; -.
DR HSSP; P02776; 1RHP.
DR MGD; MGI:188871; Pf4.
DR INTERPRO; IPR001089; -.
DR INTERPRO; IPR001811; -.
DR INTERPRO; IPR002473; -.
DR PFAM; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR PRINTS; PR00437; SMALLCYTCCX.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
DR PROSITE; 105 AA; 11243 MW; 94F0190EFA6C CRC64;
SQ

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[illegible][illegible]

	Query Match	37.3%	Score 141.5;	DB 6;	Length 101;
	Best Local Similarity	38.6%	pred. No. 3.5e-09;		
	Matches	27;	Conservative 17;	Mismatches 25;	Indels 1; Gaps 1;
Qy	3	LATELRQCLOT-LQGTHLKNIQSVKSPGPHCAQTVEIATLNKGQACLNKPASPMVYKK	61		
	:	: : :	:	: : :	: : : :
Dd	28	ISSELRCQCIKTHSTFPNPKLIKELTVIDSGPHCENSEIIKVLNNGKEVCLDPKQKWQK	87		
	62	LEKMLKNGK	71		
	:	: :			
Dd	88	VVEIFLKAAE	97		

RESULT	6
Q9QU07	
ID	PRELIMINARY; PRT; 33 AA.
AC	O9QU07
DT	01-MAY-2000 (T-EMBLrel. 13, Created)
DT	01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT	01-OCT-2000 (T-EMBLrel. 15, Last annotation update)
DE	CHEMOATTRACTANT P-3 (FRAGMENT).
OS	Rattus sp.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
QC	[1]
RN	SEQUENCE.
RP	MEDLINE=93228656; PubMed=8471066;
RX	Kanagawa H., Ikesue A., Hatakeyama S., Kato H., Gotoda T.,
RA	Nakamita N., Watanabe K., Miyai H.:
RA	"Production of an interleukin-8-like chemokine by cytokine-stimulated
RT	rat NKH-49F fibroblasts and its suppression by anti-inflammatory
RT	steroids."
RL	Biochem. Pharmacol. 45:1425-1430(1993).
RD	HSSP; P19875; LONK

DR	INTERPRO; IP0001089;	-
DR	INTERPRO; IP0001811;	-
DR	INTERPRO; IP0002473;	-
DR	Pfam; PF00048; IL8;	1.
DR	PRINTS; PR00436; INTERLEUKIN8.	
DR	PRINTS; PR00437; SMALLCYTCKXC.	
SQ	SEQUENCE	33 AA; 3561 MW; 2740F8ED16C8ClFF CRC64;
Query Match 36.1%; Score 137; DB 11; Length 33;		
Best Local Similarity 75.8%; Pred. No. 3.7e-09;		
Matches 25; Conservative 3; Mismatches 5; Indels 0; Gaps 0;		
Qy	1 APLATELRCCQLQTGGIHLKNIQSVKVKSGP 33	
Db	1 APVANELRCQCLOTVAGIHFNKIQLKVMPPGP 33	
RESULT	7	
Q9UC64	ID Q9UC64	PRELIMINARY; PRT; 54 AA.
AC	O9UC64;	
DT	01-MAY-2000 (TrEMBLrel. 13, Created)	
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)	
DE	01-OCT-2000 (TrEMBLrel. 15, Last annotation update)	
DE	PF 4-DERIVED ENDOTHELIAL CELL GROWTH INHIBITOR PEAK II (FRAGMENT)	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RA	SEQUENCE.	
RP	Gupta S.K., Hassel T., Singh J.P.;	
RL	Proc. Natl. Acad. Sci. U.S.A. 92:7799-7803(1995).	
DR	HSSP; P02776; IRRP.	
DR	INTERPRO; IP0001089;	-
DR	INTERPRO; IP0001811;	-
DR	INTERPRO; IP0002473;	-
DR	Pfam; PF00048; IL8;	1.
DR	PRINTS; PR00436; INTERLEUKIN8.	
DR	PRINTS; PR00437; SMALLCYTCKXC.	
SQ	SEQUENCE	54 AA; 6033 MW; COB560236BF1B14A CRC64;

Query Match	35.1%	Score 133;	DB 4;	Length 54;
Best Local Similarity	49.0%;	Pred. No. 1.8e-08;		
Matches	24;	Conservative 14;	Mismatches 11;	Indels 0; Gaps 0;
Qy	21	KNIOSVKVKSFGPHCAQFEVIATLKGOKACINPASPMPVKRIIEKMLN	69	
	:	: : : :	: : : : : :	: : : : : :
	:	: : : :	: : : : : :	: : : : : :
Dd	6	RHITSLEVIKAGPHCPTAOLITATLNGRKICLDLOAPLYKKIIRKLLES	54	
	:	: : : :	: : : : : :	: : : : : :
	:	: : : :	: : : : : :	: : : : : :

RESULT	8	
Q9TR91		
ID	PRELIMINARY;	48 AA.
AC	Q9TR91;	PRT;
DT	01-MAY-2000 (TREMBlrel. 13, Created)	
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)	
DT	01-OCT-2000 (TREMBlrel. 15, Last annotation update)	
DE	EPITHELIAL-DERIVED NEUTROPHIL-ACTIVATING PEPTIDE (FRAGMENT).	
OS	Bos taurus (Bovine).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;	
OC	Bovidae; Bovinae; Bos.	
OX	NCBI_TaxID=9913;	
[1]	_____	
RN	SEQUENCE.	
RP		
RX	MEDLINE=95085008; PubMed=7992841;	
RA	Allmann-Iselin I., Car B.D., Zwahlen R.D., Mueller-Schupbach R.,	
RA	Wyder-Waither M., Steckholzer U., Walz A.;	
RT	"Bovine ENA, a new monocyte-macrophage derived cytokine of the	
RT	interleukin-8 family. Structure, function, and expression in acute	

1

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Db 97 LAVDRCKVKVNRPTGLGPIIANDVIPPGIHCRTTEIIFALKKNRKVCVDPEAPWQQ 156
Qy 62 IIEKM 66
   | : |
Db 157 FIKKL 161

RESULT 12
ID O97800 PRELIMINARY; PRT; 31 AA.
AC O97800;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE EPITHELIAL CELL INFLAMMATORY PROTEIN-1 (ECIP-1) (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND INDUCTION.
RC TISSUE-KIDNEY EPITHELIUM;
RX MEDLINE=99122841; PubMed=9922392;
RA Heaton M.P., Laegreid W.W., Beattie C.W., Smith T.P.L., Kappes S.M.;
RT "Identification and genetic mapping of bovine chemokine genes
expressed in epithelial cells.";
RL Mamm. Genome 10:128-133(1999).
CC -I- INDUCTION: BY THREEFOLD IN THE PRESENCE OF LPS AND BY FOURFOLD IN
CC THE PRESENCE OF LPS AND CYCLOHEXIMIDE.
CC -I- SIMILARITY: TO GRO-GAMMA AND TO E.CABALLUS MELANOMA GROWTH
CC STIMULATORY ACTIVITY PROTEIN.
CC -I- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXCL).
DR EMBL; AF061522; AAD02809.1; -.
DR HSSP; P19875; IQNK.
DR INTERPRO; IPR001811; -.
KW PFAM; PF00048; IL8; 1.
DR Cytokine; Inflammatory response.
FT NON_TER 1
FT NON_TER 31
SQ SEQUENCE 31 AA; 3386 MW; 74172DC13D3A72B8 CRC64;

Query Match 32.5%; Score 123; DB 6; Length 31;
Best Local Similarity 74.2%; Pred. No. 1.5e-07;
Matches 23; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 43 TLKNGKACLNAPSPMVKKIIEKMLKNGSN 73
   | | | | | | | | | | | | | | | | | | | |
Db 1 TLKNGQEACLNAPSPMVKKIINKMLKNGSTN 31

RESULT 13
O93442
ID O93442 PRELIMINARY; PRT; 101 AA.
AC O93442;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE LFCA-1 PROTEIN PRECURSOR.
OS Lampetra fluviatilis (River lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Lampetra.
OX NCBI_TaxID=7748;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LEUKOCYTES;
RA Najashin A.M., Mechetina L.V., Alabyev B.Y., Taranin A.V.;
RT "Identification of the interleukin 8 homologue in lamprey (Lampetra
fluviatilis): early evolutionary divergence of chemokines.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ231072; CAA13114.1; -.
```

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DR HSSP; P02775; LTVX.
DR INTERPRO; IPR001089; -.
DR PFAM; PF00048; IL8; 1.
DR PRINTS; PR00437; SMALLCYTKXC.
KW Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 101 LFCA-1 PROTEIN.
SQ SEQUENCE 101 AA; 11095 MW; 80CFE81EA7336D2 CRC64;

Query Match 30.9%; Score 117; DB 13; Length 101;
Best Local Similarity 34.3%; Pred. No. 2.5e-06;
Matches 23; Conservative 18; Mismatches 24; Indels 2; Gaps 2;

Qy 8 RCOCLOQLT-OGIHLKNIQSVKSPGPHCAQTEVIATLKN-GOKACLNAPSPMVKKIIEK 65
   | | | | | | | | | | | | | | | | | | | |
Db 30 RCQCVHVISFIHPKHQFTMEVIPSQSNKNVEIIVTKSTNNQICLNPDAPWVRKVISH 89
   | | | | | | | | | | | | | | | | | | | |
Qy 66 MLKNGKS 72
   | : |
Db 90 ILDGAQT 96

RESULT 14
O9QV88 PRELIMINARY; PRT; 34 AA.
AC O9QV88;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE MACROPHAGE INFLAMMATORY PROTEIN 2 (FRAGMENT).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=93192044; PubMed=8383510;
RA Driscoll K.E., Hassenbein D.G., Carter J., Poynter J., Asquith T.N.,
RA Grant R.A., Whitten J., Purdon M.P., Takigiku R.;
RT "Macrophage inflammatory proteins 1 and 2: expression by rat alveolar
macrophages, fibroblasts, and epithelial cells and in rat lung after
RT mineral dust exposure.";
RL Am. J. Respir. Cell Mol. Biol. 8:311-318(1993).
DR HSSP; P10889; IMI2.
DR INTERPRO; IPR001089; -.
DR PFAM; PF00048; IL8; 1.
DR PRINTS; PR00437; SMALLCYTKXC.
SQ SEQUENCE 34 AA; 3762 MW; ECF6DD4262F44782 CRC64;

Query Match 28.5%; Score 108; DB 11; Length 34;
Best Local Similarity 61.8%; Pred. No. 9e-06;
Matches 21; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 5 TELRCQCLOTLQLOGIHLKNIQSVKSPGPHCAQT 38
   | | | | | | | | | | | | | | | | | | | |
Db 1 SELRCQCLOTLPRVDFKNIQSLVTPPGPXXAQT 34

RESULT 15
O9QV74 PRELIMINARY; PRT; 40 AA.
AC O9QV74;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE MACROPHAGE INFLAMMATORY PROTEIN 2 HOMOLOG (FRAGMENT).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
```

OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=93285151; PubMed=8508797;
RA Watanabe K., Iida M., Takaishi K., Suzuki T., Hamada Y., Iizuka Y.,
RA Tsurufuji S.;
RT "Chemoattractants for neutrophils in lipopolysaccharide-induced
RT inflammatory exudate from rats are not interleukin-8 counterparts but
RT gro-gene-product/melanoma-growth-stimulating-activity-related
RT factors.";
RL Eur. J. Biochem. 214:267-270(1993).
DR HSP; P10889; LMI2.
SQ SEQUENCE 40 AA; 4500 MW; 330DF13BAE51ACFD CRC64;

Query Match 28.2%; Score 107; DB 11; Length 40;
Best Local Similarity 59.0%; Pred. No. 1.4e-05;
Matches 23; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

OY 6 ELRCQCLOTLQIHLKNIQSVKVKSPGPHCAQTEVIATL 44
||| | : ||| : ||| | ||| |
2 ELRXQXLKTLPRVDFENIQSLTVPDPGPHXTQTEVIAAL 40

Search completed: May 4, 2001, 07:35:55
Job time: 27 sec